

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2005, 15:27:47 ; Search time 583 Seconds
(without alignments)
2275.470 Million cell updates/sec

Title: US-10-812-620-2
Perfect score: 1179
Sequence: 1 MNSTKSPASHHTRGCPKNS.....IPCFYMPWICEMPEISPLD 214

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10812620/runat_07062005_124340_3366/app_query_fasta_1.391
-DB=Published Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCU=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blom62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10812620 @CGN 1 1 624 @runat_07062005_124340_3366
-NCPU=6 -ICPU=3 -NO_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
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17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
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21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	97.5	2517	21	US-10-812-620-1 Sequence 1, Appli
2	774	968	9	9	US-09-965-529-40 Sequence 40, Appl
3	774	968	9	10	US-09-969-680A-40 Sequence 376, App
4	774	968	9	9	US-09-909-320-376 Sequence 376, App
5	774	968	9	9	US-09-909-088B-376 Sequence 376, App
6	774	968	9	9	US-09-905-291A-376 Sequence 376, App
7	774	968	9	9	US-09-902-853-376 Sequence 376, App
8	774	968	9	9	US-09-907-824-376 Sequence 376, App
9	774	968	9	9	US-09-907-841-376 Sequence 376, App
10	774	968	9	10	US-09-904-011-376 Sequence 376, App
11	774	968	9	10	US-09-903-640-376 Sequence 376, App
12	774	968	9	10	US-09-908-093-376 Sequence 376, App
13	774	968	9	10	US-09-906-742-376 Sequence 376, App
14	774	968	9	10	US-09-906-838-376 Sequence 376, App
15	774	968	9	10	US-09-907-613-376 Sequence 376, App
16	774	968	9	10	US-09-907-942-376 Sequence 376, App
17	774	968	9	10	US-09-904-859-376 Sequence 376, App
18	774	968	9	10	US-09-909-204-376 Sequence 376, App
19	774	968	9	10	US-09-904-820-376 Sequence 376, App
20	774	968	9	10	US-09-904-786-376 Sequence 376, App
21	774	968	9	10	US-09-906-646-376 Sequence 376, App
22	774	968	9	10	US-09-906-700-376 Sequence 376, App
23	774	968	9	10	US-09-903-786-376 Sequence 376, App
24	774	968	9	10	US-09-902-903-376 Sequence 376, App
25	774	968	9	10	US-09-903-749A-376 Sequence 376, App
26	774	968	9	10	US-09-904-119-376 Sequence 376, App
27	774	968	9	10	US-09-904-956-376 Sequence 376, App
28	774	968	9	10	US-09-902-736-376 Sequence 376, App
29	774	968	9	10	US-09-907-794-376 Sequence 376, App
30	774	968	9	10	US-09-903-943-376 Sequence 376, App
31	774	968	9	10	US-09-904-462-376 Sequence 376, App
32	774	968	9	10	US-09-907-925-376 Sequence 376, App
33	774	968	9	10	US-09-902-692-376 Sequence 376, App
34	774	968	9	10	US-09-903-520-376 Sequence 376, App
35	774	968	9	10	US-09-905-056-376 Sequence 376, App
36	774	968	9	10	US-09-909-064-376 Sequence 376, App
37	774	968	9	10	US-09-904-553-376 Sequence 376, App
38	774	968	9	10	US-09-905-381-376 Sequence 376, App
39	774	968	9	10	US-09-904-485-376 Sequence 376, App
40	774	968	9	10	US-09-905-348-376 Sequence 376, App
41	774	968	9	10	US-09-905-088-376 Sequence 376, App
42	774	968	9	10	US-09-907-575-376 Sequence 376, App
43	774	968	9	10	US-09-905-075-376 Sequence 376, App
44	774	968	9	10	US-09-902-759-376 Sequence 376, App
45	774	968	9	10	US-09-902-634-376 Sequence 376, App

ALIGNMENTS

RESULT 1
US-10-812-620-1
; Sequence 1, Application US/10812620
; Publication No. US20050019860A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; TITLE OF INVENTION: A novel C-type lectin and its genes
; FILE REFERENCE: J9904071
; CURRENT APPLICATION NUMBER: US/10/812.620
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/10/110.945
; PRIOR FILING DATE: 2002-04-14
; PRIOR APPLICATION NUMBER: JP 11-293724
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1

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; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Mouse
US-10-812-620-1

Alignment Scores:
Pred. No.: 1.4e-135 Length: 2517
Score: 1149.00 Matches: 209
Percent Similarity: 98.13% Conservative: 1
Best Local Similarity: 97.66% Mismatches: 4
Query Match: 97.46% Indels: 0
DB: 21 Gaps: 0

US-10-812-620-2 (1-214) x US-10-812-620-1 (1-2517)

QY 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 124 ATGAATTCACCAAAATCGGCTGCATCCACACACAGAGAGGATGCTTCAAAAACCTCC 183
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 184 CAAGTGCTCTCTCGACAGATAGCGGGGCTCATCTCTGTTCTCAGTGGCTGTTTCATC 243
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
Db 244 ACCAGATGTGCTGACATATCGACGCTCTCAAAATTCGGGCGAGAACTTACAGCCACAT 303
QY 61 ArgAsnIleGlyGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCysCys 80
Db 304 AGAAATATTAAGAGAGCTTTCCTGCTACAGTGAGGCATCAGGTTCAAGAAATGCTGT 363
QY 81 ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr 100
Db 364 CCTTTGAATCGAAACATTATCAATCTAGTTGTTATTTTCTCTACGACAACTTGACC 423
QY 101 TrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
Db 424 TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGGCTCACTGGTGGTTATCGACACA 483
QY 121 GlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
Db 484 CAGGAAGAGCAGAGAAATTCCTTTTCGCACAAAAATCTAAAGAGAAAGAGTTTATATGGA 543
QY 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
Db 544 CTGACACAGCAGGTGGTGGAGGTCAGTGGCAATGGGAGGATGATACACTTTTCACAGAG 603
QY 161 SerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCysAla 180
Db 604 TCCTGGACCTTCGGGATGCTGGGAGGCCCAACAATATAGTTTGGTGGAGGACTGTGCC 663
QY 181 ThrIleArgAspSerSerAenSerArgLysAenTrpAsnAspIleProCysPheTyrSer 200
Db 664 ACCATAAGGAGACTCTTCAAACTCCAGGAAGAACTGGAATGATAAATCCCTGTTTCTACAGT 723
QY 201 MetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 724 ATGCCCTTGGATTGTGAGATGCCAGAAATAAGTCTCTCAGGAC 765

RESULT 2
US-09-965-529-40
; Sequence 40, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: PATTERSON, Chandra
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; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 1521513CB1
US-09-965-529-40

Alignment Scores:
Pred. No.: 2.82e-88 Length: 968
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 9 Gaps: 2

US-10-812-620-2 (1-214) x US-09-965-529-40 (1-968)

QY 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 162 ATGAATTCATCTAAATCATCTGAAACACAATGCACAGAGAGGATGCTTC---TCTTCC 218
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 219 CAATGTCTTATGGACTGTGCTGGGATCCCCATCCTATTCTCAGTGCCTGTTTCATC 278
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 279 ACCAGATGTGTGTGACATTTTCGCATCTTCAACCTCTGTATGAGAAAAAGTTTCAGCTA 338
QY 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
Db 339 CCTGAGAATTTTCACAGAGCTCTCTCTGCTACAAATATATGATCGATCAGGTTCAAGAATGT 398
QY 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 399 TGTCCATTTGAATCGGAATATTTTCAATCCAGCTCTACTCTTCTTCTACTGACACCAAT 458
QY 100 ThrTrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 459 TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC 518
QY 120 ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 519 TCACAGGAGGAGCAGAGAAATTCCTTTTCTTACAAAGAAACCTAAATGAGAGAGTTTATTT 578
QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 579 GGACTGTTCAGACCCAGGTTGTGAGGGTCAGTGGCAATGGGTGGACGGCACACCTTTTGACA 638
QY 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 639 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGGCCCAACAATAGCTACCTGGAGGACTGT 698
QY 180 AlaThrIleArgAspSerSerAenSerArgLysAenTrpAsnAspIleProCysPheTyr 199
Db 699 GCCACCATGAGAGACTCTTCAAACTCCAAAGGCAAAATTTGGAATGATGTAACCTGTTTCTC 758
QY 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 759 AATTATTTTCGGATTGTGAAATGTTAGGAATAAATCTCTTTGAAC 803

RESULT 3
US-09-969-680A-40
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; Sequence 40, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dyrung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 1521513CB1
US-09-969-680A-40

Alignment Scores:
Pred. No.:      2,82e-88      Length:      968
Score:          774.00        Matches:    143
Percent Similarity: 79.07%   Conservative: 27
Best Local Similarity: 66.51% MisMatches:     43
Query Match:      65.65%     Indels:       2
DB:              10         Gaps:        2

US-10-812-620-2 (1-214) x US-09-969-680A-40 (1-968)

Qy      1 MetAsnSerThrIysSerProAlaHisThrGluArgGlyCysPheLeuAsnSer 20
Db      162 ATGAATTCATCTAAATCATCTCTGAAACACAAATGCAGAGAGAGGATGTTCC---TCTTCC 218

Qy      21 GluValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheile 40
Db      219 CAAATGTCTTATGGACTGTCTGGGATCCCCATCTATTCTCAGTGCGCTGTTTCATC 278

Qy      41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db      279 ACCAGATGTGTGTGCATATTCGCCATCTCTTCAAACCTGTGTGATGAGAAAAAGTTTCAGCTA 338

Qy      60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
Db      339 CTGAGAATTTTCACAGAGCTCTCCGTCAATAATTTGATGATCAGGTTCAGTCAAGAAATGT 398

Qy      80 CysProLeuAsnTrpIysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db      399 TGTCATTTGACTGGGAATATTTTCAATCCAGCTGCTACTCTTTCTTACTCACACCATT 458

Qy      100 ThrTrpSerSerSerLeuIysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db      459 TCCTGGCGGTAAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGTGTGTTATCAAC 518

Qy      120 ThrGlnGluGlnGlnGluPheLeuPheArgThrIysProLysArgLysGluPheTyrlle 139
Db      519 TCACAGAGAGAGCAGAAATTCCTTTCTCCTCAAGAACCTTAATATGATGAGAGATTTTTTAT 578

Qy      140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThr 159
Db      579 GGACTGTTCAGACACAGGTTGTTCAGGGGTGAGTGGCAATGGGTGGACGGCACACCTTTGACA 638

Qy      160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179

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; Sequence 40, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dyrung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 1521513CB1
US-09-969-680A-40

Alignment Scores:
Pred. No.:      2,82e-88      Length:      968
Score:          774.00        Matches:    143
Percent Similarity: 79.07%   Conservative: 27
Best Local Similarity: 66.51% MisMatches:     43
Query Match:      65.65%     Indels:       2
DB:               10         Gaps:        2

US-10-812-620-2 (1-214) x US-09-969-680A-40 (1-968)

Qy      1 MetAsnSerThrIysSerProAlaHisThrGluArgGlyCysPheLeuAsnSer 20
Db      162 ATGAATTCATCTANATCATCTCGAAACACAAATCCAGAGAGAGGAGTCTTC---TCITCC 218

Qy      21 GluValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheile 40
Db      219 CAAATGTCTTATGGACTGTCTGGGATCCCCATCTATTCTCAGTGCCGTGTTTCATC 278

Qy      41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db      279 ACCAGATGTGTGTGCACATTCGCCATCTCTTCAAACTGTGTGATGAGAAAAAGTTTCAGCTA 338

Qy      60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
Db      339 CTGAGAATTTTCACAGAGCTCTCCGTCAATAATTTAGGATCAGGTTCAGTCAAGAAATGT 398

Qy      80 CysProLeuAsnTrpIysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db      399 TGTCATTTGACCTGGGAATATTTCAATCCAGCTGCTACTCTTTCTTACTCACACCATT 458

Qy      100 ThrTrpSerSerSerLeuIysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db      459 TCCTGGCGGTAAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGCTGTGTATCAAC 518

Qy      120 ThrGlnGluGlnGlnGluPheLeuPheArgThrIysProLysArgLysGluPheTyrlle 139
Db      519 TCACAGAGAGAGCAGAAATTCCTTTCTCCTCAAGAACCTTAATAATGACGAGAGTTTTTATT 578

Qy      140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThr 159
Db      579 GGACTGTACAGACAGGTTGTTCAGGGGTGAGTGGCAATGGGTGGACGGCACACCTTTTGACA 638

Qy      160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179

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Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 9 Gaps: 2

US-10-812-620-2 (1-214) x US-09-909-088B-376 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACAATGACAGAGAGAGATGCTTC---TCTTCC 162

Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheLe 40
Db 163 CAAATGTTCTTATGGAGCTGTGTGGATCCCATCTATTCTCAGTGGCTGTTTCATC 222

Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGACATTCGATCTTCAACCTGTGATGAGAAAAGTTTCAGCTA 282

Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCGAGAAATTCACAGAGCTCTCTCTGCTACAAATATGATGATCAGGTTTCAGTCAAGAAATTGT 342

Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTTGAACCTGGGAATATTTTCAATCCAGCTGCTACTCTTTCTACTGACACCAT 402

Qy 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 403 TCCGGGCGGTAAAGTTAAAGAACTCTCAGCCATGGGGCTACCTGGTGGTTATCAAC 462

Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACGAGGAATTCCTTCTCACAAGAAACCTTAAATGAGAGAGATTTTATT 522

Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTGACAGCAGGTTGTGAGGGTTCAGTGGCAATGGGTGGACGCACACCTTTTGACA 582

Qy 160 GluSerLeuSerPheTrpAspAlaGlyProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTCTGGGATGTAGGGGAGCCCAACACATAGCTACCTGGAGGAGCTGT 642

Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAACCCCAAGGCACAAATTTGGAATGATGTAACCTGTTCTC 702

Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGGATTTCTGAAATGTTAGGAATAAATCCTTTGAAC 747

RESULT 6

US-09-905-291A-376
; Sequence 376, Application US/09905291A
; Patent No. US20020160374A1

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavina, Ivar J.

; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-905-291A-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 9 Gaps: 2

US-10-812-620-2 (1-214) x US-09-905-291A-376 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACAATGACAGAGAGAGATGCTTC---TCTTCC 162

Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheLe 40
Db 163 CAAATGTTCTTATGGAGCTGTGTGGATCCCATCTATTCTCAGTGGCTGTTTCATC 222

Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59

Db 223 ACCAGATGTTGTGACATTTCCGATCTTTCAAAACCTGTGATGAGAAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CTTGAGAAATTTACAGAGCTCTCTGCTCAATATGGAATTCAGTTCAGTCAAGAATTGT 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 343 TGTCCATTTGAACTGGAAATATTTCAATCCAGCTGCTACTCTTTTCTACTGACCACTT 402
Qy 100 ThrTrpSerSerLysLeuLysAsnCysSerAspMetGlyAlaHisLeuValValLysAsp 119
Db 403 TCTGGCGCTTAAGTTTAAAGAACTGCTCAGCATGGGGGCTCACCTGGTGTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGGAATTCCTTCTCTCAAGAAACCTAAATAGAGAGATTTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GACTGTCTACAGACAGTTGTCAGGGTCAGTGGCAATGGTGGACGGCACCTTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTCTGGGATGTAGGGAGCCCAACATAGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATTTGAATGATGTAACTGTTTCCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGGATTTGTGAAATGTAGGAATAAATCTTTGAAC 747

RESULT 7

US-09-902-853-376
; Sequence 376, Application US/09902853
; Publication No. US20020192859A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-853-376
Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 9 Gaps: 2
US-10-812-620-2 (1-214) x US-09-902-853-376 (1-997)
Qy 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAAATTCATTAATCATCTGAAACACAAATGCACAGAGAGGATGTTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCATCTATTTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTTTCGATCTTTCAAAACCTGTGATGAGAAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CTTGAGAAATTTACAGAGCTCTCTGCTCAATATGGAATTCAGTTCAGTCAAGAATTGT 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 343 TGTCCATTTGAACTGGAAATATTTCAATCCAGCTGCTACTCTTTTCTACTGACCACTT 402
Qy 100 ThrTrpSerSerLysLeuLysAsnCysSerAspMetGlyAlaHisLeuValValLysAsp 119
Db 403 TCTGGCGCTTAAGTTTAAAGAACTGCTCAGCATGGGGGCTCACCTGGTGTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139

Db 463 TCACAGGAGGACAGGAATTCCTTCTTACAGAAACCTAAATGAGAGATTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTTCAGACCAAGTTGTCTGAGGGTTCAGTGGCAATGGTGGACGGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCAACACATAGCTACCTCGAGGAGCTGT 642
Qy 180 AlaThrIleArgAspSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACGAGAGACTCTTCAAAACCCAGGAGGCAATGGAAATGATGTAACCTGTTTCCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGATTTGTGAATGGTAGGATAAATCCTTTGAAC 747

RESULT 8

US-09-907-824-376
; Sequence 376, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-824-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 9 Gaps: 2

US-10-812-620-2 (1-214) x US-09-907-824-376 (1-997)

Qy 1 MetaAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACACAATGACAGAGAGAGATGCTTC---TCITCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTGCGCATCTTTCAAACCTGTGTATGAGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAAATTTCAACAGAGCTCTCTCTGCTACAATTTATGGATCAGGTTCAAGAAATGT 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAACCTGGGAATATTTTCATCCAGTCTACTCTTTCTTCTACTGACACCAT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 403 TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGGAAATTCCTTTCTACAAGAAACCTAAATATGAGAGAGATTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTACAGCCAGGTTGTGAGGGTTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCAACACATAGCTACCTCGAGGAGCTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACATGAGAGACTCTTCAAACCCAGGCAAAATTTGGAATGATGTAACCTGTTTCCTC 702

QY 200 SerMetProTripleCysGluMetProGluIleSerProLeuAasp 214
 Db 703 AATTATTTTCGGATTGTGAAATGGTAGGAATAAATCCTTTGAAC 747

RESULT 9

US-09-907-841-376
 ; Sequence 376, Application US/09907841
 ; Publication No. US20020198366A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/907,841
 ; PRIOR FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 376
 ; LENGTH: 997
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-09-907-841-376

Alignment Scores:
 Pred. No.: 2,95e-88 Length: 997
 Score: 774.00 Matches: 143
 Percent Similarity: 79.07% Conservative: 27
 Best Local Similarity: 66.51% Mismatches: 43

Query Match: 65.65% Indels: 2
 DB: 9 Gaps: 2
 US-10-812-620-2 (1-214) x US-09-907-841-376 (1-997)
 QY 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAasnSer 20
 Db 196 ATGAATTCATCTAAATCATCTGAAACACAATGCACAGAGAGAGGATGCTTC--TCTTCC 162
 QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 Db 163 CAAATGTTCTTATGGACTGTGCTGGATCCCATCTTATTTCTCAGTGCCTGTTTCATC 222
 QY 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln--AsnLeuGlnPro 59
 Db 223 ACCAGATGTGTGTGACATTTTCCGATCTTTCAACCTGTGATGAGAAAAAGTTTCAGCTA 282
 QY 60 HisArgAsnIleLysGluLeuSerCysTyArgSerGluAlaSerGlySerValLysAasnCys 79
 Db 283 CCTGGAATTTACAGAGCTCTCTGCTACAAATATGATGATGAGTTCAATCAAGATTGT 342
 QY 80 CysProLeuAasnTrpLysHisTyArgSerSerCysTyArgPhePheSerThrThrThrLeu 99
 Db 343 TGTCCATTGAATCGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAT 402
 QY 100 ThrTrpSerSerSerLeuLysAasnCysSerAspMetGlyAlaHisLeuValValIleAasp 119
 Db 403 TCCTGGGGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCCTGGTGTATCAAC 462
 QY 120 ThrGlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyIle 139
 Db 463 TCACAGAGGAGCAGGAAATTCCTTCTTCAAGAAACCTTAAATCAGAGAGTTTATT 522
 QY 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAlaAspAspThrProPheThr 159
 Db 523 GGACTGTTCAGACCAGGTTGTGAGGGTCAGTGGCAATGGTGGCGGACGACACCTTTGACA 582
 QY 160 GluSerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAaspCys 179
 Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTGGAGGACTGT 642
 QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAasnTrpAasnAspIleProCysPheTy 199
 Db 643 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATGGAATGATGTAACCTGTTTCCTC 702
 QY 200 SerMetProTripleCysGluMetProGluIleSerProLeuAasp 214
 Db 703 AATTATTTTCGGATTGTGAAATGGTAGGAATAAATCCTTTGAAC 747

RESULT 10

US-09-904-011-376
 ; Sequence 376, Application US/09904011
 ; Publication No. US20030003530A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James

```

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904.011
; CURRENT FILING DATE: 2001-07-11
; PRIOR FILING DATE: 2000-09-18
; PRIOR FILING DATE: 2000-02-22
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-28
; PRIOR FILING DATE: 1999-09-08
; PRIOR FILING DATE: 1999-09-13
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-11-30
; PRIOR FILING DATE: 1999-12-02
; PRIOR FILING DATE: 1999-12-02
; PRIOR FILING DATE: 1999-12-02
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-011-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservatives: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

US-10-812-620-2 (1-214) x US-09-904-011-376 (1-997)

Qy 1 MethSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTTCATTAATCATCTCTGAACACAAATGCACAGAGAGAGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAATGTCTTATGAGACTCTCTGGGATCCCAATCTATCTTCAGTGGCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59

223 ACCAGATGTGTGTGACATTTCCGCAATCTTTCAACCTGTGATGAGAAAAAGTTTCAGCTA 282
60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
283 CCTGAGAAATTTCCAGAGCTCTCTCTGTACAAATATATGATCAGGTTTCTAGTCAAGAAATGT 342
80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
343 TGTCCATTGAATGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAATT 402
100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
403 TCCTGGCGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTTATCAAC 462
120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
463 TCACAGGAGGAGCAGGAAATTCCTTCTACAGAAACCTAAATGAGAGAGATTTTATT 522
140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
523 GGAATGTGACAGACCAAGGTTTGTGAGGGTCAATGGGTGGAGCGGCACACCTTTTGACA 582
160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnIleValLeuValGluAspCys 179
583 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACCAACATAGCTACCTCGAGGACTGT 642
180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
643 GCACCATGAGAGACTCTTCAACCCCAAGCAAAATTTGGAATGATGATTAACCTGTTTCTC 702
200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
703 AATTATTTTCGGATTTCGTAATGGTAGGAATAAATCCTTTTGAAC 747

RESULT 11
US-09-903-640-376
; Sequence 376, Application US/09903640
; Publication No. US20030017463A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903.640
; CURRENT FILING DATE: 2001-07-11
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
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; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-640-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservatives: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

US-10-812-620-2 (1-214) x US-09-903-640-376 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysHisSer 20
Db 106 ATGAATTCATCTAAATCATCTCGAACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerThrThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGAGCTCTCTCGGATCCCATCTTATCTCAGTCGCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTTCCGATCTTCAAACTGTGATGAGAAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysHisCys 79
Db 283 CCTGAGAATTTCCACAGAGCTCTCTGCTACAAATATGATGATCAGGTTTCAGTCAAGAATTGT 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 343 TGTCCATTTGAATCGGAATATTTTCAATCCAGCTGCTACTCTTTCTTACTGACACCAATT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 403 TCCTGGCGGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGCTGTTATCAAC 462
Qy 120 ThrGlnGluGlnGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACAGGAATTCCTCTCTCAAGAAACCTTAAATGAGAGAGTTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnThrGlnTrpValAspAspThrProPheThr 159
Db 523 GGAGTGTTCAGACAGCGGTTGTGAGGGTTCAGTGGCAATGGTGGCGGACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACATAGTACCTCGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAAACCAAGGCAAAATGGAATGATGTAACCTGTTTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGATTGTGAAATGTAGGAATAAATCCTTTTGAAC 747

RESULT 12

US-09-908-093-376
; Sequence 376, Application US/09908093
; Publication No. US20030017498A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/908,093
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-908-093-376

Alignment Scores:

Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservatives: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

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US-10-812-620-2 (1-214) x US-09-908-093-376 (1-997)
Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACACAAATGCACAGAGAGAGATGCTTC--TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCATCTCTATTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTCCGATCTTTCAACCTGTGTATGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
Db 283 CCTGAGAATTTTCACAGAGCTCTCTGCTACAAATATTGATGATCAGGTTCAAGAAATGT 342
Qy 80 CysProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAACTGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAAT 402
Qy 100 ThrTrpSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 403 TCCCTGGGGTTAAGTTTAAAGACTCTCAACCCATGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGGAATCTCTTCTCAAGAAACCTAAATCAGAGAGTTTATTAT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTGCAGACCAAGTTGTGAGGGTCAAGTGGCAATGGGTGGAGCGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAenIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAenTrpAenAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAAACCAAGGCAAAATGGATGATGATGAACCTGTTCTTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC 747

RESULT 13
US-09-906-742-376
; Sequence 376, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
```

```
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-742-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

US-10-812-620-2 (1-214) x US-09-906-742-376 (1-997)
Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACACAAATGCACAGAGAGAGATGCTTC--TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCATCTCTATTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTCCGATCTTTCAACCTGTGTATGAGAAAAGTTTCAGCTA 282
```

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QY 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
Db 283 CTGAGAAATTTACAGAGCTCTCTGCTACAAATATGATCAGTTTCAGTCAAGATGTT 342
QY 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAATCGGGAATATTTCAATCCAGCTGCTACTTCTTTTCTACTGACACCAT 402
QY 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 403 TCCTGGCGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCCTGGTGTATCAAC 462
QY 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACAGGAATTCCTTCTCCTACAGAAACCTTAAATGAGAGATTTTATT 522
QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThr 159
Db 523 CGACTGTACAGACAGGTTCTGAGGGTCAAGTGGCAATGGTGGACGGCACACCTTTGACA 582
QY 160 GluSerLeuSerPheThrAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCGGGATGTAGGGGAGCCCAACATAGCTACCCCTGGAGGACTGT 642
QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCACCATGAGAGATCTTCAACCCAGGCAAAATTTGAATGATGTAACTGTTTCCTC 702
QY 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGGATTTGTGAATGGTAGGAATAAATCCTTTCGAAC 747

RESULT 14
US-09-906-838-376
; Sequence 376, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
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; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-838-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

US-10-812-620-2 (1-214) x US-09-906-838-376 (1-997)
QY 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAATATCATCTGAAACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCATCTATTTCTCAGTGCCTGTTTCATC 222
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTTCGATCTTTCAAACCTGTGTGATGAGAAAAGTTTCAGCTA 282
QY 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
Db 283 CCTGAGAAATTTACAGAGCTCTCTGCTACAAATATGATCAGTTTCAGTCAAGATGTT 342
QY 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAATCGGGAATATTTCAATCCAGCTGCTACTTCTTTTCTACTGACACCAT 402
QY 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 403 TCCTGGCGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCCTGGTGTATCAAC 462
QY 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCTGAGGAGGACAGGAATTCCTTCTCCTACAGAAACCTTAAATGAGAGATTTTATT 522
QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThr 159
Db 523 CGACTGTACAGACAGGTTCTGAGGGTCAAGTGGCAATGGTGGACGGCACACCTTTGACA 582
QY 160 GluSerLeuSerPheThrAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCGGGATGTAGGGGAGCCCAACATAGCTACCCCTGGAGGACTGT 642
QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCACCATGAGAGATCTTCAACCCAGGCAAAATTTGAATGATGTAACTGTTTCCTC 702
QY 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGGATTTGTGAATGGTAGGAATAAATCCTTTCGAAC 747
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Db		463	TCAAGGAGGACAGGAATTCCTTCC	TACAAGAAACCTAAATGAGAGAGTTTATT	522
Qy		140	GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr	159	
Db		523	GGACTGTCAAGACCAGGTTGTGCAGGGTCAGTGCGCAATGGGTGACGGCACACCTTTTGACA	582	
Qy		160	GluSerLeuSerPheTrpAspAlaGlyCyluProAsnAsnIleValLeuValGluAaspCys	179	
Db		583	AAGTCTCTAGAGTCTTCTGGGATGTATGGGGAGGCCAACACATAGCTACCCCTGGAGGACTGT	642	
Qy		180	AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr	199	
Db		643	GCACCATGAGAGACTCTTCAAACCCAGGCAAAATTTGGAAATGATGTAACTGTTTCCTC	702	
Qy		200	SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp	214	
Db		703	AATATTTTTCCGATTTGTGAATGTGTAGGAATAAATCTTTTGAC	747	

RESULT 15

US-09-907-613-376
; Sequence 376, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29

Db 703 AATTATTTTCGGATTGTGAAATGGTAGGAATAAATCCTTTGAAC 747

Search completed: June 9, 2005, 17:44:27
Job time : 594 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2005, 03:50:51 ; Search time 420 Seconds
(without alignments)
9805.973 Million cell updates/sec

Title: US-10-812-620-1
Perfect score: 2517
Sequence: 1 cggctgttactcttgaaact.....aaataaagtaataaactatt 2517

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
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- 6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	439.4	17.5	997	4	US-09-907-794A-376
2	439.4	17.5	997	4	US-09-905-125A-376
3	439.4	17.5	997	4	US-09-902-775A-376
4	439.4	17.5	997	4	US-09-906-700-376
5	439.4	17.5	997	4	US-09-903-603A-376
6	439.4	17.5	997	4	US-09-904-920A-376
7	439.4	17.5	997	4	US-09-909-064-376
8	439.4	17.5	997	4	US-09-905-361A-376
9	439.4	17.5	997	4	US-09-906-618-376
10	157.8	6.3	301	3	US-09-222-575-29
11	157.8	6.3	301	4	US-09-389-681-29
12	157.8	6.3	301	4	US-09-620-405B-29
13	157.8	6.3	301	4	US-09-339-338-29
14	157.8	6.3	301	4	US-09-433-826B-29
15	157.8	6.3	301	4	US-09-604-287A-29
16	157.8	6.3	301	4	US-09-285-480-29
17	157.8	6.3	301	4	US-09-834-759-29
18	157.8	6.3	301	4	US-09-590-751A-29
19	157.8	6.3	301	4	US-09-551-621-29
20	95.8	3.8	334	4	US-09-016-434-698
21	94.8	3.8	1104	3	US-09-111-470-1
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24	83.6	3.3	169334	4	US-09-949-016-15999
25	82	3.3	99370	4	US-09-949-016-12816
26	82	3.3	99370	4	US-09-949-016-17540
27	82	3.3	144158	4	US-09-949-016-11755

Sequence 12936, A
Sequence 14724, A
Sequence 14577, A
Sequence 14578, A
Sequence 41762, A
Sequence 41761, A
Sequence 15691, A
Sequence 15450, A
Sequence 12008, A
Sequence 17056, A
Sequence 15968, A
Sequence 8, Appl
Sequence 51, Appl
Sequence 16415, A
Sequence 17504, A
Sequence 14353, A
Sequence 17590, A
Sequence 14095, A

ALIGNMENTS

RESULT 1

US-09-907-794A-376

; Sequence 376, Application US/09907794A

; Patent No. 6635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Geritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; PRIOR FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 376
 ; LENGTH: 997
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-09-902-775A-376

Query Match 17.5%; Score 439.4; DB 4; Length 997;
Best Local Similarity 72.9%; Pred. No. 6.9e-105;
Matches 610; Conservative 0; Mismatches 216; Indels 11

	Matches	610;	Conservative	0;	Mismatches	216;	Indels	11;	Gaps	3
Qy	87	AGAGAAGAAAGGAAGAAAGCGCAGGAAAAAGGAAGTAATGAATTCAACCAAATCCCTGC	146							
Db	69	AGAGAGAGAGAAAACAIAAIIIIICAAAGAGAGAGAAAAATGAATTCATCTAAATCATCTCGA	128							
Qy	147	ATCCCCACACACAGAGAGAGATGCTTCAAAAATCTCCCAAGTGCTCTCTCGAGCGATAGC	206							
Db	129	AACAAATGCACAGAGAGAGATGCTTC---TCITCCCAATGTCTTATGGACTGTGGC	185							
Qy	207	CGGGCCCTCCATCTCTGTTTCTCAGTGGCTGTGTTTCATCACAGATGTGTGCTGAACATATCG	266							
Db	186	TGGGATCCCCATCTATTCTCAGTGCCTGTTTTCATCACAGATGTGTTGTGACATTTTCG	245							
Qy	267	CAGCTCTCAA--TTTCCGGGCGAGACTTACAGGCCATAGAAATATTAAAGGAGCTTTC	323							
Db	246	CATCTTTCAAACCTGTGATGAGNAAAAAGTTTCAGCTACCTCAGAAATTTTCAGAGAGCTCTC	305							
Qy	324	CTGCTACAGTGAAGGCATCAGGTTCAGTCAAGAAATGCTGTCCTTTGAACTCGGAAACATTA	383							
Db	306	CTGCTACANTTATGGATCAGGTTTCAGTCAAGAAATGTTGTTCATTGAATCGGGAATATT	365							
Qy	384	TCAATCTAGTTGTTATTTTTTCTCTACGACAACTTGTACCTGGTCAACAAGTTTAAAGAA	443							
Db	366	TCAATCCAGCTGCTACTCTTTTCTACTGACACCATTTCCTGGCGTTTAAAGTTTAAAGAA	425							
Qy	444	TTGCTCAGACATGGGGCTCACCTGGTGGTTATCGACACAGAGAGCAGGAAATTCCT	503							
Db	426	CTGCTCAGCCATGGGGCTCACCTGGTGGTTATCAACTCAAGAGGAGCAGGAATTCCT	485							
Qy	504	TTTTTCGACAAAATCTAAAAGAAAGAGTTTTATATTGGAAGTGCAGACACAGGCTGGTGGGA	563							
Db	486	TTCTCAAGAAACCTTAAATGAGAGAGTTTTTTTATTGGACTGTGACACAGGTTGTCGA	545							
Qy	564	GGTCACTGGCAATGGGAGGATGATACACTTTTCACAGAGTCCCTGACCTTCGGGATGC	623							
Db	546	GGGTCACTGGGCAATGGGTGGACGGCACACTTTGACAAAGTCTCTGAGCTTCTGGGATGT	605							
Qy	624	TGGGAGCCCAACAATATAGTTTTGGTGGAGGACTGTGCCACCATAAGGGAGCTCTTCAA	683							
Db	606	AGGGAGCCCAACAATAGCTACCTCGAGAGACTGTGCCACCATGAGAGACTCTTCAAA	665							
Qy	684	CTCCAGGAAGAACTGGAAATGATAATCCTCTGTTCTTACAGTAGTCCCTTGGATTTGTGAGAT	743							
Db	666	CCCAAGGCAAAATTTGGAATGATGAACCTGTGTTCTCTCAATTTATTTTCGGAATTTGTGAAAT	725							
Qy	744	GCCAGAATTAAGTCTCAGGACTAAGTGCAA-----GGAAATACAGGGACATGGCTTAC	798							
Db	726	GGTAGGAATAAATCCTTTGAAACAAGGAAATATCTCTTTAAGAACAGAGGCAACAATCCA	785							
Qy	799	ATGCATGAAGAAGAAACAAGAGTGAATGTATAACAACCAAAATCCAACATAAGAAAAATAT	858							
Db	786	ATGTGTAAAGAAAGNAGAGCAAGAACATGGGCCACACCCGCCCCACACAGGAAATTTG	845							
Qy	859	CTATCAGGCATCAGAAGACTGCGCATGTATGTATTACTGGGACANAAGTAAAAAGA	915							
Db	846	TGCGCTGAACCTTCAAGAGCTTCATAAGTATTTGTTACTCTGATCAAAATAAAAAATA	902							

RESULT 4
US-09-906-700-376
; Sequence 376, Application US/09906700
; Patent No. 6723535

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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-906-700-376
Query Match 17.5% Score 439.4 DB 4 Length 997

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Query Match 17.5%; Score 439.4; DB 4; Length 997;


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Db 666 CCCAAGGCAAAATTGGAATGATGTAACCTGTTTCTCAATATTTTCGGATTGTGAAAT 725
Qy 744 GCAGAAATAGTCTCAGGACTAGTGCAA-----GGAAATACAGGACATGGCTTAC 798
Db 726 GGTAGGAATAAATCTCTTTGAACAAAGAAAATCTCTTTAAGAACAGAGGCGCAACTCAA 785
Qy 799 ATGCATGAAGAAGAACAAAGAGTGAATGTAATAACCAACCAAAATCCAACATAAGAAAATAT 858
Db 786 ATGTGTAAGAAGAAAGAGACAGACATGGCCACACCCACCGCCACACGAGAAATTG 845
Qy 859 CTATCAGGCATCAGAAAGACTGCACATGTATGTATTACTTGGACATAAGTAAAAAGA 915
Db 846 TCGCTGTAACCTTCAAAGGACTTCATAAGTATTGTTACTCTGATACAAATAAAAAATA 902

RESULT 10
US-09-222-575-29/c
; Sequence 29, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-29
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Query Match 6.3%; Score 157.8; DB 3; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGAGTGGTGGAGGTCAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTACAGACAGGTTGTCAGAGGTCAGTGGCAATGGGAGGATGATACACC 242
Qy 594 TTTCACAGAGTCCCTGACCTTCTGGGATCTGGGAGGCCCAACAATATATATTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATCTGGGAGGCCCAACAATATAGTACCTGGA 182
Qy 654 GGACTGTGCCACCAATAGGAGCTTCAAACTCCAGGAAGAACTGGAATGATAATCCCTG 713
Db 181 GGACTGTGCCACCAATAGGAGCTTCAAACTCCAGGAAGAACTGGAATGATAATCCCTG 122
Qy 714 TTTCACAGATGCGCTTGGATTGTGAGATGCCAGAAATAAGTCTCAGGACTAAAGTGA 773
Db 121 TTTCTCAATATTATTTTCGGATTGTGAAATGTTAGGAATTAATCTTTGAACAAAGGAAA 62

Qy 774 A 774
Db 61 A 61
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RESULT 11
US-09-389-681-29/c
; Sequence 29, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
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; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-29
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Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGAGTGGTGGAGGTCAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTACAGACAGGTTGTCAGAGGTCAGTGGCAATGGGAGGATGATACACC 242
Qy 594 TTTCACAGAGTCCCTGACCTTCTGGGATCTGGGAGGCCCAACAATATATATTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATGTTAGGAGGCCCAACAATAGTACCTGGA 182
Qy 654 GGACTGTGCCACCAATAGGAGCTTCAAACTCCAGGAAGAACTGGAATGATAATCCCTG 713
Db 181 GGACTGTGCCACCAATAGGAGCTTCAAACTCCAGGAAGAACTGGAATGATAATCCCTG 122
Qy 714 TTTCACAGATGCGCTTGGATTGTGAGATGCCAGAAATAAGTCTCAGGACTAAAGTGA 773
Db 121 TTTCTCAATATTATTTTCGGATTGTGAAATGTTAGGAATTAATCTTTGAACAAAGGAAA 62

Qy 774 A 774
Db 61 A 61
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RESULT 12
US-09-620-405B-29/c
; Sequence 29, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-29
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Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGAGTGGTGGAGGTCAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTACAGACAGGTTGTCAGAGGTCAGTGGCAATGGGAGGATGATACACC 242
Qy 594 TTTCACAGAGTCCCTGACCTTCTGGGATCTGGGAGGCCCAACAATATATATTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATGTTAGGAGGCCCAACAATAGTACCTGGA 182
Qy 654 GGACTGTGCCACCAATAGGAGCTTCAAACTCCAGGAAGAACTGGAATGATAATCCCTG 713
```

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Db 181 GGACTGTGCCACCATGAGAGACTTCAAAACCCCAAGGCAAAATTTGGAATGATGTAACCTG 122
Qy 714 TTTCTACAGTATGCTTGGATTCTTGAGATGCCAGAAATAGTCTCAGGACTAAGTGCA 773
Db 121 TTTCCTCAATTTTTCGGATTGTGAAATGTTAGGAATAAATCCTTTGAACAAGGAAA 62
Qy 774 A 774
Db 61 A 61

RESULT 13
US-09-339-338-29/c
; Sequence 29, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-339-338-29
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Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGTGGTGGAGGGTCAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTCAGACCAGGTGTTCGAGGGTCAGTGGCAATGGGAGGATGATACACC 242
Qy 594 TTTCACAGAGTCCCTGACCTTCTGGGATGCTGGGAGGCCCAACAATATAGTTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATGTTAGGGAGGCCCAACAATATAGTTAACTCG 182
Qy 654 GGACTGTGCCACCATAGGAGACTCTTCAAACTCCAGGAAGAACTGGGAATGATAATCCCTG 713
Db 181 GGACTGTGCCACCATGAGAGACTCTTCAAAACCCCAAGGCAAAATTTGGAATGATGTAACCTG 122
Qy 714 TTTCTACAGTATGCTTGGATTGTGAGATGCCAGAAATAGTCTCAGGACTAAGTGCA 773
Db 121 TTTCCTCAATTTTTCGGATTGTGAAATGTTAGGAATAAATCCTTTGAACAAGGAAA 62
Qy 774 A 774
Db 61 A 61
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RESULT 14
US-09-433-826B-29/c
; Sequence 29, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
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; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-433-826B-29
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Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
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Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGTGGTGGAGGGTCAGTGGCAATGGGAGGATGATACACC 593
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

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Listing first 45 summaries

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13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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VERSION	E54035.1	GI:22553489			
KEYWORDS	JP 2001112482-A/1.				
SOURCE	Mus sp.				
ORGANISM	Mus sp.				

REFERENCE 1 (bases 1 to 2517)
AUTHORS Shinra,S. and Matsumoto,M.
TITLE Novel C lectin and gene thereof
JOURNAL Patent: JP 2001112482-A 1 24-APR-2001;
COMMENT OS Mus sp. (mouse)
PN JP 2001112482-A/1
PD 24-APR-2001
PF 15-OCT-1999 JP 1999293724
PI SHIZUO SHINRA, MAKOTO MATSUMOTO
PC C12N15/09,A61K38/00,A61P31/00,A61P37/04,A61P43/00,C07K14/47,
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FEATURES
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Key Location/Qualifiers

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DEFINITION
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VERSION BD094039.1 GI:22639627
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SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Akira,S. and Matsumoto,M.
AUTHORS A novel C-type lectin and its genes
TITLE Patent: WO 0127271-A 1 19-APR-2001;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP, SHIZUO AKIRA, MAKOTO MATSUMOTO
COMMENT OS Mus sp. (mouse)
PN 'WO 0127271-A/1
PD 19-APR-2001
PF 02-OCT-2000 WO 2000JP006820
PR 15-OCT-1999 JP 99P 293724
PI SHIZUO AKIRA, MAKOTO MATSUMOTO
PC C12N15/12, C07K14/47, C12Q1/68, A61K38/17, A61P31/00, A61P37/04, PC
A61P43/00
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FH Key Location/Qualifiers.
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Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	2281	AAAC	CTGA	GTG	ATCAT	AGAT	AACTTT	TGG	ATCTTT	TG	2340
Db	2281	AAAC	CTGA	GTG	ATCAT	AGAT	AACTTT	TGG	ATCTTT	TG	2340
Qy	2341	AAAC	ATG	ACCC	AAAA	ACTAT	CTTGG	CGGG	AAAA	TTTTAA	2400
Db	2341	AAAC	ATG	ACCC	AAAA	ACTAT	CTTGG	CGGG	AAAA	TTTTAA	2400
Qy	2401	CTATTT	TAGAA	TTG	GAC	AGTGG	GGGA	ATCAT	CC	AAATTTG	2460
Db	2401	CTATTT	TAGAA	TTG	GAC	AGTGG	GGGA	ATCAT	CC	AAATTTG	2460

Qy	2461	TGTACATTAGGTTACAGAAAAACAACCTTTAGCCACAAAAATAAAGTAATAAACTATT	2517
Db	2461	TGTACATTAGGTTACAGAAAAACAACCTTTAGCCACAAAAATAAAGTAATAAACTATT	2517
RESULT 3			
AB024717			
LOCUS			
DEFINITION	AB024717 Mus musculus mRNA for macrophage C-type lectin Mincle, complete cds.	2517 bp	mRNA linear ROD 10-NOV-1999
ACCSSION	AB024717		
VERSION	AB024717.1	GI:5821285	
KEYWORDS	Mincle; macrophage C-type lectin Mincle.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Matsumoto,M., Tanaka,T., Kaisho,T., Sanjo,H., Copeland,N.G., Gilbert,D.J., Jenkins,N.A. and Akira,S.		
TITLE	A novel LPS-inducible C-type lectin is a transcriptional target of NF-IL6 in macrophages		
JOURNAL	J. Immunol. 163 (9), 5039-5048 (1999)		
MEDLINE	99458965		
PUBMED	10528209		
REFERENCE	2 (bases 1 to 2517) pub. 11/1/99		
AUTHORS	Akira,S. and Matsumoto,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-MAR-1999) Shizuoka Akira, Osaka University, Department of Host Defense, Research Institute for Microbial Diseases; 3-1 Yamada-oka, Suita, Osaka 565-0871, Japan		
(E-mail:sakira@iken.osaka-u.ac.jp, Tel.:81-6-6879-8303, Fax:81-6-6879-8305)			
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ORIGIN			
Query Match	98.9%; Score 2489.8;	DB 10;	Length 2517;
Best Local Similarity	99.3%;	Pred. No. 0;	
Matches 2500;	Conservative 0;	Mismatches 17;	Indels 0; Gaps 0;
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Db 601 GAGTCCCTGAGCTTCTGGGATGCTGGGAGGCCCAACAATATAGTTTGGTGGAGACTGT 660
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RESULT 4
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 LOCUS AC124563 210092 bp DNA linear ROD 25-NOV-2003
 DEFINITION Mus musculus BAC clone RP23-206B15 from chromosome 6, complete
 sequence.
 ACCESSION AC124563
 VERSION AC124563.4 GI:33300796
 KEYWORDS HTG
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 210092)
 Abbott, S. and Meyer, R.
 TITLE The sequence of Mus musculus BAC clone RP23-206B15
 JOURNAL Unpublished (2001)
 REFERENCE 2 (bases 1 to 210092)
 AUTHORS Wilson, R.
 TITLE Sequencing of Mus musculus
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 210092)
 AUTHORS McPherson, J.D. and Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 4 (bases 1 to 210092)
 McPherson, J.D. and Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (15-APR-2003) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 5 (bases 1 to 210092)
 Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (29-JUL-2003) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 6 (bases 1 to 210092)
 Wilson, R.
 TITLE Direct Submission
 JOURNAL Submitted (25-NOV-2003) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jul 29, 2003 this sequence version replaced gi:29837778.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu
 Contact: submission@watson.wustl.edu
 ----- Summary Statistics
 Center project name: M_BA0206B15

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. Wea Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see

http://genome.wustl.edu

SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.reagen.com) or Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

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repeat_region	21606..21751
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McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smalls, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Warra, M. A.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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Matches 1579; Conservative 0; Mismatches 16; Indels 1; Gaps 1;	
Qy	43 CACCATTCAAGACTCAGCTTTCCAGGGGCTCTTTCTAAACTGAGAGGAAGAAAGGAA 102
Db	1 CACCATTCAAGACTCAGCTTTCCAGGGGCTCTTTCTAAACTGAGAGGAAGAAAGGAA 60
Qy	103 GAAAGGCGAGGAAAGGAGAAATGAATTCACACCAAAATCGCCTGCATCCACACACAGAG 162
Db	61 GAAAGGCGAGGAAAGGAGAAATGAATTCACACCAAAATCGCCTGCATCCACACACAGAG 120
Qy	163 AGAGGATGCTTTCAAAACTCCCAAGTCTCTCTGGAGCATAGCGGGGCTCCATCCTG 222
Db	121 AGAGGATGCTTTCAAAACTCCCAAGTCTCTCTGGAGCATAGCGGGGCTCCATCCTG 180
Qy	223 TTTCTCAGTGGCTGTTTCATCACCAGATGTGTCTGTAACATATCGCAGCTCTCAAAATTTCC 282
Db	181 TTTCTCAGTGGCTGTTTCATCACCAGATGTGTCTGTAACATATCGCAGCTCTCAAAATTTCC 240
Qy	283 GGGCAGAACTTACAGCCACATAGAAATTAATTAAGGAGCTTTCTCGTACAGTGAGGCAATCA 342
Db	241 GGGCAGAACTTACAGCCACATAGAAATTAATTAAGGAGCTTTCTCGTACAGTGAGGCAATCA 300
Qy	343 GGTTCAGTCAAGAAATGCTGTCTTTGAACCTGGAACATTAATCAATCTAGTTGTATTTT 402
Db	301 GGTTCAGTCAAGAAATGCTGTCTTTGAACCTGGAACATTAATCAATCTAGTTGTATTTT 360
Qy	403 TTCTCTACGACAACTTTGACCTGTGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGCT 462
Db	361 TTCTCTACGACAACTTTGACCTGTGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGCT 420
Qy	463 CACTGTGTGTTATCGACACACAGAGAGCAGGAAATTCCTTTTTCGCACAAAATCTAAA 522
Db	421 CACTGTGTGTTATCGACACACAGAGAGCAGGAAATTCCTTTTTCGCACAAAACCTAAA 480
Qy	523 AGGAAAGGTTTTATATGGAAGTCAACAGCAGCTGGTGGAGGCTCAGTGCATGGGAG 582
Db	481 AGGAAAGGTTTTATATGGAAGTCAACAGCAGCTGGTGGAGGCTCAGTGCATGGGAGT 540
Qy	583 GATGATACACTTTTCACAGAGTCCCTGACCTTTCTGGGATGCTGGGGAGCCCAACAATATA 642
Db	541 GATGATACACTTTTCACAGAGTCCCTGACCTTTCTGGGATGCTGGGGAGCCCAACAATATA 600
Qy	643 GTTTTGTGGAGGACTGTGCCACCATAGGAGCTCTTCAAACCTCAGAGAAATCTGGAAT 702
Db	601 GTTTTGTGGAGGACTGTGCCACCATAGGAGCTCTTCAAACCTCAGAGAAATCTGGAAT 660
Qy	703 GATAATCCCTGTTCTACAGTATGCTTGGATTTGTGAGATGCCAGAAATTAAGTCTCTCAG 762
Db	661 GATAATCCCTGTTCTACAGTATGCTTGGATTTGTGAGATGCCAGAAATTAAGTCTCTCAG 720
Qy	763 GACTAAGTGCAGGAAATACAGGACATGCTTTACATGATGAAGAGAAACAAGAGTGA 822
Db	721 GACTAAGTGCAGGAAATACAGGACATGCTTTACATGATGAAGAGAAACAAGAGTGA 780
Qy	823 ATGTAATAACAAACCAAAATCCAAATAGAAATATCTATCAGGACATCAGAGGAGCTGCA 882
Db	781 ATGTAATAACAAACCAAAATCCAAATAGAAATATCTATCAGGACATCAGAGGAGCTGCA 840
Qy	883 CATGTATGTATTACTGGGACATAGTAAAGACTTGTTCCTATGCTTAAAGTCCACAG 942
Db	841 CATGTATGTATTACTGGGACATAGTAAAGACTTGTTCCTATGCTTAAAGTCCACAG 900
Qy	943 CATTTGTCTGATGGTCTTGCCATAACCTCGAAAGATCTCTTTTACAGTGTACAGATCAATT 1002
Db	901 CATTTGTCTGATGGTCTTGCCATAACCTCGAAAGACTCTTTTACAGTGTACAGATCAATT 960
Qy	1003 CTCTAACAAATGCAACAGAGAAAGGAAATCTCTTTTTCACATCTGTCTTTGACATCTG 1062
Db	961 CTCTAACAAATGCAACAGAGAAAGGAAATCTCTTTTTCACATCTGTCTTTGACATCTG 1020
Qy	1063 TCTTGCTCATGAGAAATGATATGAAGGAGGAGTAGAAAGCAGATGTCTGTATTAAGAGA 1122
Db	1021 TCTTGCTCATGAGAAATGATATGAAGGAGGAGTAGAAAGCAGATGTCTGTATTAAGAGA 1080

Qy	1123 CTTTAAATGGTCACTATGTCATCTCTGTTCTTTCTACATCCTTGGCTCTAGCTTATCTATCT 1182
Db	1081 CTTTAAATGGTCACTATGTCATCTCTGTTCTTTCTACATCCTTGGCTCTAGCTTATCTATCT 1140
Qy	1183 ATCAGTACATAGATCACTCTCTGTTCTTCCACAGTGGAGAGATGCATCTTTGAGTCTT 1242
Db	1141 ATCAGTACATAGATCACTCTCTGTTCTTCCACAGTGGAGAGATGCATCTTTGAGTCTT 1200
Qy	1243 TAAACTTACCTCGCGCTTGGAGAAATGGCATGGCTTTCAGCAAGGACATCTCCATATGGA 1302
Db	1201 TAAACTTACCTCGCGCTTGGAGAAATGGCATGGCTTTCAGCAAGGACATCTCCATATGGA 1260
Qy	1303 AAGGCCGGTCAAACTTCAGTTCCTTAACAGATTTGATCTAGTCCACCTCTTCTCGAGGCC 1362
Db	1261 AAGGCCGGTCAAACTTCAGTTCCTTAACAGATTTGATCTAGTCCACCTCTTCTCGAGGCC 1320
Qy	1363 CATTTTCTCTGTGTTCTCTTCTATATAAAGTGGATTTACCTGTACTTGTATCTACTCGCA 1422
Db	1321 CATTTTCTCTGTGTTCTCTTCTATATAAAGTGGATTTACCTGTACTTGTATCTACTCGCA 1380
Qy	1423 AGTAGAACCTGCTCAGTAGGTTCAAGTGAAATTTATTTAAAAATTCATGTTTCAATTTT 1482
Db	1381 AGTAGAACCTGCTCAGTAGGTTCAAGTGAAATTTATTTAAAAATTCATGTTTCAATTTT 1440
Qy	1483 CTGTCTCAGGACTGCTATTTATTTGATGATATTTCTGTCATATAGACCATGTTTCTTCCAG 1542
Db	1441 CTGTCTCAGGACTGCTATTTATTTGATGATATTTCTGTCATATAGACCATGTTTCTTCCAG 1500
Qy	1543 ACAAGGCCATTAGGAA-CTTCAGCAGCAGTCACACATTTGTAATAAATGATGATCTTGA 1601
Db	1501 ACAAGGCCATTAGGAAACCTTCAGCAGCAGTCACACATTTGTAATAAATGATGATCTTGA 1560
Qy	1602 GTAGGAAATTAACCTAAATAAATTTGTCATA 1637
Db	1561 GTAGGAAATTAACCTAAATAAATTTGTCATA 1596

RESULT 6	
AC109882	
LOCUS	222035 bp DNA linear HTG 11-OCT-2002
DEFINITION	Rattus norvegicus clone CH230-310L5, *** SEQUENCING IN PROGRESS
	***, 4 unordered pieces.
ACCESSION	AC109882
VERSION	AC109882.4 GI:23607730
KEYWORDS	HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 222035) Muzny,D.Marié., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Blawlo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, X., London, P., Longacre, S., Lopez, J., Loresushewa, L., Loulsegod, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montenayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munitasa, M., Murphy, M., Naif, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puaor, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlaczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, E., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

Direct Submission
2 (bases 1 to 222035)
Worley, K.C.

Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 222035)

Rat Genome Sequencing Consortium.

Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Oct 9, 2002 this sequence version replaced gi:21744187.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GQJU

Center clone name: CH230-310L5

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 202672 bases at least Q40

Consensus quality: 204982 bases at least Q30

Consensus quality: 206533 bases at least Q20

Estimated insert size: 208212; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 7987: contig of 7987 bp in length
* 7988 8087: gap of unknown length
* 8088 11519: contig of 3432 bp in length
* 11520 175535: gap of unknown length
* 175536 175535: contig of 163916 bp in length
* 175536 175535: gap of unknown length
* 175536 222035: contig of 46400 bp in length.

FEATURES

source

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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-310L5"

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misc_feature

/note="wgs contig"

6646..7987

misc_feature

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8088..9437

misc_feature

/note="wgs contig"

9488..11519

misc_feature

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131182..132689

misc_feature

/note="wgs contig"

complement(161303..162152)

misc_feature

/note="clone_boundary"

clone end: T7

site: MboI

end_sequence: RXALO63TJ"

ORIGIN

Query Match	46.6%	Score 1173;	DB 2;	Length 222035;
Best Local Similarity	80.5%	Pred. No. 6.5e-238;		
Matches 1557;	Conservative 0;	Mismatches 335;	Indels 43;	Gaps 14;
QY	606	CCTGACCTTCGGGATGCTGGGGAGCCCAACAATAGTTTTGGTGGAGGACTGTGCCAC	665	
Db	18755	CCACAGCTTCGGGATGCTGGAGAGCCCAATACATAGTTTTGGTGGAGGACTGTGCCAC	18814	
QY	666	CATAAGGGACCTTCAAACTCCAGGAAGAACTGGAAATGATAATCCCTGTTCTACAGTAT	725	
Db	18815	CATGAGGACCTTCAAACTCCAGGAAGAACTGGAAATGATAATCCCTGTTCTACAGTAT	18874	
QY	726	GCCTTGGATTGTGAGATGCCAGAAATAGTCTCAGGACTAAGTCAAGGAATACAG	785	
Db	18875	GCCTTGGATTGTGAGATGCCAGAAATAGTCTTGGACTAGGTGCAAGGAACACAGA	18934	
QY	786	GGACATGCGCTTACATGCAATGAAGAAGAACAGAGTGAATGTATAACCAACCAAAATCCAA	845	
Db	18935	AGACATGTTTACATGCAATGAAGAAGAACAGAGTGAATGTATAACCAACCAAAATCCAA	18994	
QY	846	CATAAGAAATATCTATCAGGCATCAGAGGACTGCACATGTATGTATTTACCTGGGACATA	905	
Db	18995	CACAAGAAATGGCTGTCTGGGCATCAGAAAGGCCACATATGTATGTATTATGAATA	19054	
QY	906	AGTAAAGA-CTTGTTCCCATGCTTAAAGTCCACAGCATTTGTCTGATGGTCTTGCCAT	964	
Db	19055	AGTAAATGAGTGTCTTCCATGGCTTAAATCCACAGAAATCATCTGACGTTCTGCCAT	19114	
QY	965	AACTGAAAGATCTCTTTTAGACTGTACAGATCAATTTCTTAAACAAATGCAACGAAG	1024	
Db	19115	AACTGAAAGTCTCTTTTCAATATACAAAGCAATCTCTTAATAATGACGACAGACA	19174	
QY	1025	AAAGGATTCCTCTTTTCAATCTCTTTGCAATCTGTTGCTCATGAG-----A	1076	
Db	19175	AAAGGATTCCTCTTTTCAATCTCTTTTCCCAAGGGAATTTGATATGAAGGAGGATTA	19234	

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ORIGIN	Query Match Best Local Similarity 22.8%; Score 574.4; DB 10; Length 730; Matches 627; Conservative 0; Mismatches 69; Indels 3; Gaps 1;
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QY	402 TTTCTCTACGACAACTTGACCTGGTTCATCAAGTTTAAAGAAATTTGCTCAGACATGGGGC 461
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QY	462 TCACCTGGTGGTATCGACACAGGAAGAGGAAATTCCTTTTCGCACAAAATCTAA 521
Db	392 TCACCTGGTGGTATCAACACATGGAAGAGGAAATTCCTTTTCGCACAAAACCCAG 451
QY	522 AAGGAAGATTTTATATGGAAGTACAGACACAGGTTGGGGTTCAGTGGCAATGGGA 581
Db	452 AAGGAAGATTTTATATGGAAGTACAGACACAGGTTGGGGTTCAGTGGCAATGGGT 511
QY	582 GGATGATACACCTTTTCACAGAGTCCCTGACCTTCTGGGATGCTGGGGAGCCCAACAAT 641
Db	512 GGATGATACACCTTTTCACAGAGTCCCTGACCTTCTGGGATGCTGGAGAGCCCAATACAT 571
QY	642 AGTTTGGTGGAGACTGTGCCACCATAAAGGACTCTTCAAACTCCAGGAAGACTGGAA 701
Db	572 AGTTTGGTGGAGACTGTGCCACCATGAGGAGCTCTTCAAAACCCAGGAAGAACTGGAA 631
QY	702 TGATATCCCTGTTCTACAGTATGCTTGGATTTGAGATGCCAGAAATAGTCCTCA 761
Db	632 TGATATCCCTGTTCTTACAGTATGCTTGGATTTGAGATGCCAGAAATAGTCCTTT 691
QY	762 GGAATAGTCAAGGAAATACAGGAGCATGGCTTACAT 800
Db	692 GGAATAGTCAAGGAAACACAGAGACATGGTTTACAT 730

RESULT 8	
CQ717831	2144 bp DNA Linear PAT 03-FEB-2004
LOCUS	Sequence 3765 from Patent WO02068579.
DEFINITION	CQ717831
ACCESSION	CQ717831.1 GI:42278688
VERSION	
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE	Kits, such as nucleic acid arrays, comprising a majority of human exons or transcripts, for detecting expression and other uses

thereof
Patent: WO 02068579-A 3765 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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QY	147 ATCCACACACACAGAGAGGATGCTTCAAAAACCTCCCAAGTGTCTCTCGACGATAGC 206
Db	175 AACCAATGACAGAGAGAGGATGCTTC---TCITCCCAATGTTCTTATGAGACTGTTGC 231
QY	207 CGGGCCCTCCATCTCTGTTTCTCAGTGGCTGTTTCATACACAGATGTGCTAAACATGCG 266
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QY	324 CTGCTACAGTGAAGGATCAGGTTTCAGTCAAGAAATTCCTTCTTGAATTCGAAACATTA 383
Db	352 CTGCTACAAATATTGATCAGGTTTCAGTCAAGAAATTCCTTCTTGAATTCGAAATATT 411
QY	384 TCAATCTAGTTGTTATTTTCTCTACGACAACTTCGACCTGGTGTCTCAAGTTTAAAGAA 443
Db	412 TCAATCCAGCTGCTACTTCTTCTTCTACGACCACTTTCTGGGCGTTAAAGTTAAAGAA 471
QY	444 TTGCTCAGACATGGGGCTCAGCTGGTGTTCAGACACAGAGAGAGGAGGAAATTCCT 503
Db	472 CTGCTCAGCCATGGGGCTCAGCTGGTGTTCATCAACTCAGAGGAGGAGGAAATTCCT 531
QY	504 TTTTCGCACAAAATCTAAAGGAAAGAGTTTATATTGGAAGTTCAGACACAGGAGGAGTGTGA 563
Db	532 TTCTTACAGAAACCTAAATAGAGAGAGTTTATATTGGAAGTTCAGACAGGAGTGTGCGA 591
QY	564 GGGTCAGTGGCAATGGGAGGATGATACACCTTTTCAAGAGTCCCTGACCTTCTGGGATGC 623
Db	592 GGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGT 651
QY	624 TGGGAGAGCCCAACATATAGTTTGGTGGAGGAGTGTGCCACCATAGGAGACTCTTCAA 683
Db	652 AGGGAGAGCCCAACACATAGCTTACCTTGGAGGAGTGTGCCACCATAGGAGACTCTTCAA 711
QY	684 CTCCAGGAAGAACTGGAATGATTAATCCCTGTTTCTACAGTATGCTTGGATTTGTGAGAT 743
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QY	744 GCCAGAAATAGTCTCTCAGGACTAAGTGCAA-----GGAAATACAGGAGACATGCTTAC 798
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QY	799 ATGCAATGAAGAAGAAACAGAGTGAATTAATACCAACCAATTCACACATAGAAATAT 858
Db	832 ATGTGTAAGAAGGAAGAGCAAGAACATGGCCACACCCACCGCCCCACACAGGAATTTG 891
QY	859 CTATCAGGCATCAGAAGGAGCTGCATGTATGTTTACTTGGGACATATAGTAAAGAGCTT 918
Db	892 TCGCGTGAACCTCAAGGAGCTTCATAGTATTTGTTACTCTGATATTAATAAATATAGT 951
QY	919 GTTCCCATTTGCTAAAGGCTCCACAGCATTTGCTGATGG-----TCITGCCATACCTG 970
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1012 CAGGTCCTCTTCCAGAGATTTTACAAAGCAATTCATCTACCTTTTGTCTACATTTGGCTC 1068
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Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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1249 CTGCCAAGCATATATCGTCTTTTACTCCCTGTATATAGTAAAGAGCTTCTTCAAG 1308
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1239 TCTTTAACTTACCTCGCGCTGGAGAAATGGCATGGCTT-----CAGCAAG 1286
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1309 TCATGAACTTA-TTCCTGCTCAGAAATACCGGTGTGGCTTCTGGCTACAGGCTCCAC 1367
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1287 GACATCTCCATATGGAAGCGCGTCAAACTTCAGTTCTCTTAACAGATTTGTGATCTAGTCC 1346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1347 ACTC-TTCCTGGAGCCCATTTTCTCTGTCTTCTCTCTCTATAAC-----TGTATTTACCC 1401
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1428 ACCATCCCTGGGCTCTCTTGTCTGCTCTTATTTTCAATTTGACTGAATGGATCTCACC 1487
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1402 TGTACTTGTATCTACTGCGCAAGTAGACCTGCTCAGTAGGTTCAAAAGTGAATTTATTA 1461
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1488 AGATTTTGTATCTATGCTCAGTAGGACCGAGTCCAAATAGTCAAT-TTATTTAAGCG 1546
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1547 AACATTCATCCACACTTTCTCTGTCTCAAGCC 1579

RESULT 9
AC113782
LOCUS
DEFINITION Rattus norvegicus clone CH230-97B16, *** SEQUENCING IN PROGRESS
AC113782 linear HTG 15-NOV-2002
***, 5 unordered pieces.
AC113782
VERSION AC113782.6 GI:25006612
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 246843)
Muzny,D,Marie., Metzker,M, Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,M., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,X., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,K., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.B., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Detamo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,W.,
Gebregiorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
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Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
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Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
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Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwakalemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Platter,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smaje,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Umami,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiser,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 246843)
Worley,K.C.
Direct Submission
Submitted (05-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246843)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23267207.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GSGL
Center clone name: CH230-97B16
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 214283 bases at least Q40
Consensus quality: 217684 bases at least Q30
Consensus quality: 220184 bases at least Q20
Estimated insert size: 222530; sum-of-contigs estimation
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Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 32891: contig of 32891 bp in length
* 32892 32991: gap of unknown length
* 32992 241925: contig of 208934 bp in length
* 241926 242025: gap of unknown length
* 242026 243303: contig of 1278 bp in length
* 243304 243403: gap of unknown length
* 243404 244454: contig of 1051 bp in length
* 244455 244554: gap of unknown length
* 244555 246843: contig of 2289 bp in length.

FEATURES

source

1. 246843

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end sequence:BH279502"

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/note="wgs_contig"

ORIGIN

Query Match 18.1%; Score 456.6; DB 2; Length 246843;
Best Local Similarity 71.3%; Pred. No. 26-86;
Matches 580; Conservative 0; Mismatches 224; Indels 9; Gaps 4;

QY 1711 TACAATAATATCTTACACACACATTTGACTTCTCTTTTAAAAATTAATTTTGTGAA 1770
DB 32890 TTTNN 32949

QY 1771 AATTTGTGCATTTATATTAATCTACTTTAATGAACCCATCTTACTCTCTCTACTACAA 1830
DB 32950 NNN 33009

QY 1831 CTGTCTCTTATCCACTCACTGATTTTCCCTCCCAATTTTCATGTCTCTCTCTTTT 1890
DB 33010 TCTGCCCTTTCACCTCACTGTTTTCCTGACAAATTCATGTCTCTCTTTTGTGTTTA 33069

QY 1891 AACCCACTCTATCTGTCTAGTCTCTCTGAAATGCACTTGAGTATAGGCTTTCTACTGGA 1950
DB 33070 AACCTATTATGTCCTCACTCACTGCTTCTGAAATGCACTTGAGTATAGGCTTTCTACTGGA 33129

QY 1951 CC----ATAGCTCTGGGCAACACATCCCACTCTCCACTCTCCAGCAGGGAACAATA 2006
DB 33130 ACATAGATAGCGTCTCAGAAACACATCCCACTCTCCACTCTCCAGCAGGGAACAATA 33189

QY 2007 GCAATGACCATCTTTCAGCT--GAGGATGATTTTCATGAGTCCCATGCTCATGCTGG 2065
DB 33190 ACCAATGATTAATCTTCACTGGAGTGGAATTTCAATGATTTTCATGCTCATGCTGG 33249

QY 2066 AATTTGGGTGTTTATGTAACCTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2125
DB 33250 AATTTGGGATGTTTCCATGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 33309

QY 2126 TCTTAGGAGCTTCATATTAAGAATTCGAATTCATCAAAAGGGGACACAAAGAAATCA 2185
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DB 33487 CTTTGTGATGTTTCCACTTTTCTATTGCTGTGATGACACATAGGCCAAAAGAGCTTGG 33546
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DB 33667 ACTTTAGTCACAAAATAGGGTAGTAAGCCAGT 33699

RESULT 10
CQ414662
LOCUS CQ414662 2143 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21733 from Patent WO0170979.
ACCESSION CQ414662
VERSION CQ414662.1 GI:41322443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 21733 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
source 1. 2143
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 18.1%; Score 456.2; DB 6; Length 2143;
Best Local Similarity 62.3%; Pred. No. 3.9e-86;
Matches 915; Conservative 0; Mismatches 488; Indels 66; Gaps 10;

QY 87 AGAAGGAAAAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 146
DB 115 AGAGAGAGAGAAACAAAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 174

QY 147 ATCCACACACAGAGAGAGGATGCTTCAAAAACCTCCCAAGTGTCTCTCTGGACGATAGC 206
DB 175 AACCAATGACAGAGAGAGGAGGATGCTTCTTCTCCCAATGTTCTTATGAGCTGTTGC 231

QY 207 CGGGGCTCCATCTGTTTCTCAGTGGCTGTTTCTATCACAGATGTCGTAACATATCG 266
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QY 267 CAGCTCTCAAA---TTTCCGGGCGAGACTTACAGCCACATAGAAATATTAAGGAGCTTTC 323
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QY 324 CTGCTACAGTGAGGATCAGGTTTCAGTCAAGATTTGCTCTTGTAACTGGAACATTA 383
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Db	352	 CTGCTACAATTTATGGATCAGGTTTCAGTCAAGAAATTTGTTGCCATTGGAATCTGGGAATATTT	411
Qy	384	TCAATCTAGTTGTTATTTTCTCTACGACAAACCTTCGACCTGGTGCATCAAGATTTTAAAGAA	443
Db	412	 TCAATCAGCTGCTACTCTCTTTCTACTGACACCAATTTCTTGGCGGTTTAAAGTAAAGAA	471
Qy	444	TTGCTCAGACATGCGGGCTCACCTGGTGGTTATCGACACACAGAGAGCAGGAATTCCT	503
Db	472	CTGCTCAGCCATGCGGGCTCACCTGGTGGTTATCAACTCAGGAGGAGCAGGAATTCCT	531
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Db	892	TGCGCTGAACCTTCAAAGGACTTCTAAGTATTTGTTTACTCTGTATATAATAAAAAATAAGT	951
Qy	919	GTTCCTCATGTCTAAAGTCCACACATTTGCTGATGG- - - - -TCGTGCCATAACCTG	970
Db	952	AGTTTTAAATGTTATAATTCAATGTTCTGGCTGAAGTGCAATTTCTCTCTACGTTAGTCT	1011
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Qy	1211	CCA- - - - -ACAGTGAGGAAGATGCATCTTTGAGTCCT	1242
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Qy	1243	TAAACTTACCTCGCGCTGGGAGAAATGGCATGGGCTT- - - - -CAGCAAGACA	1290
Db	1312	GAAACTTA- TTCTTGCTCAGAAATACCGGTGTGGCTTTCTTGGCTACAGGGCTTCACATGCA-	1370
Qy	1291	TCTCCATATGAAAAGGCGGTCAAACTTCAGTTCTTAACAGATTTGATCTAGTCCCACTC	1350

Db	1371	CCTTCTTAGGGAAGGCGATGCCAGCCATCAGCTCCAAACAGGCTGTAAACCAAGTCACCC	1430
Qy	1351	TTCCCTGGAGCCCATTTCTCTGTGTCTCTCTATATAAC----	1405
Db	1431	ATCCCTGGGGCTTCCTTTGTCTGTGCCTTATTTTCAATTGACTGAATGGATCTCACCAGAT	1490
Qy	1406	CTTGTATCTACTGCGCAAGTAGAACCTGCTCAGTAGGTTCAAAGTGAATATTTTAAAAA	1465
Db	1491	TTTGTATCTATTGCTCAGCTAGGACCCGAGTCCCAATAGTCAATTT-ATTCTAAGCGAACA	1549
Qy	1466	TTCAATGTTTCACATTTTCTGTCTCAGGAC	1494
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DEFINITION			Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9, mRNA (cdna clone MGC:1246 IMAGE:3507103), complete cds.
ACCESSION			BC000715
VERSION			BC000715.2 GI:33875777
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SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
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AUTHORS			1 (bases 1 to 927)
			Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Klausner,R.D., Collins,F.S., Zeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,B., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Vallon,D.K., Muny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,M.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE			Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL			Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED			12477932
AUTHORS			2 (bases 1 to 927)
TITLE			Strausberg,R.
JOURNAL			Direct Submission
			Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK			NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT			On Aug 19, 2003 this sequence version replaced gi:12653848.
			Contact: MGC help desk
			Email: gcaps-x@mail.nih.gov
			Tissue Procurement: DCTD/DTF
			cDNA Library Preparation: Rubin Laboratory
			cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
			DNA Sequencing by: Institute for Systems Biology
			http://www.systembiology.org
			contact: amadan@systembiology.org
			Anup Madan, Jessica Fahy, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
			Clone distribution: MGC clone distribution information can be found

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ACCESSION	BD172543		
VERSION	BD172543.1 GI:28413845		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
JOURNAL	the same		
COMMENT	PATENT: JP 2002223786-A 316 13-AUG-2002; GENENTECH INC		
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24-NOV-1997 US	60/066770, 24-NOV-1997 US	60/066511	PR
24-NOV-1997 US	60/066453, 25-NOV-1997 US	60/066840	PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI			
JIAN ZHENG,			
PI JEAN YUAN			
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC			
C12N5/10,			
PC			
C12P21/02//C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC			
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Db	546	GGGTGAGTGGCAATGGGTGGACGGCACACCTTTTGACAAAGTCTCTGAGCTTCTCGGGATGT	605
QY	624	TGGGAGGCCCAACAATATAGTTTGGTGGAGGACTGTGCCACCATAAGGACTCTTCAA	683
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Job time : 10831 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2005, 02:18:26 ; Search time 1325 Seconds
(without alignments)
11245.275 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	456.2	18.1	2143	12	Ado24494 Human PRO
4	441	17.5	968	4	Aaf81743 Human mem
5	441	17.5	976	10	Adf90738 Human hep
6	441	17.5	990	7	Adr41300 Human CD-
7	439.4	17.5	997	2	Aax52274 Protein P
8	439.4	17.5	997	3	Adc78688 Human PRO
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ALIGNMENTS

RESULT 1
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ID AAF86349 standard; cdna; 2517 BP.
XX AC AAF86349;
XX AC AAF86349;
DT 23-JUL-2001 (first entry)
XX DE Murine cDNA encoding C-type lectin Mincle.
KW Mouse; Mincle; C-type lectin; antiinflammatory; macrophage; inflammation;
KW immune disorder; nuclear factor interleukin 6; NF-IL6; BB.
OS Mus sp.
XX FH Key Location/Qualifiers
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FT /note= "C-type lectin"
XX PN WO200127271-A1.
XX PD 19-APR-2001.
XX PF 02-OCT-2000; 2000WO-JP006820.
XX PR 15-OCT-1999; 99JP-00293724.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX Akira S, Matsumoto M;
XX WPI; 2001-273771/28.
XX P-PSDB; AAB97225.
XX New macrophage activating C-type lectin for the treatment of immune disorders and inflammation.
XX Claim 4; Fig 4; 60pp; Japanese.
XX This invention relates to a C-type lectin, termed Mincle, which is formed from a transcriptional target gene of nuclear factor interleukin 6 (NF-

CC	IL6). Mincle is a macrophage activating protein which can be used in the									
CC	treatment of immune disorders, and inflammation. Compositions containing									
CC	the protein have immunomodulatory and antiinflammatory activity. The									
CC	present sequence represents murine cDNA encoding Mincle									
XX										
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Qy	661	GCCACCATAGGAGACTCTTTCAAATCCAGGAGAACTGGGAATGATAATCCCTGTTTCTAC	720							
Db	661	GCCACCATAGGAGACTCTTTCAAATCCAGGAGAACTGGGAATGATAATACCCTGTTTCTAC	720							
Qy	721	AGTATGCCCTTGGATTTGTGAGATGCCAGAAATAAAGTCTTCAGGACTCAAGTGAAGAAAT	780							
Db	721	AGTATGCCCTTGGATTTGTGAGATGCCAGAAATAAAGTCTTCAGGACTCAAGTGAAGAAAT	780							
Qy	781	ACAAGGGACATGGCTTACATGATGAAGAGAACCAAGAGTGAATGTAATACCAACAAA	840							
Db	781	ACAAGGGACATGGCTTACATGATGAAGAGAACCAAGAGTGAATGTAATACCAACAAA	840							
Qy	841	TCCACATTAAGAAATATCTATCAGGCATCAGAGGACTGCACATGTATGTATTACTGGG	900							
Db	841	TCCACATTAAGAAATATCTATCAGGCATCAGAGGACTGCACATGTATGTATTACTGGG	900							
Qy	901	ACATAAGTAAAAAGACTTGTTCCTTCCATTGCTTAAAGTCCACAGCATTTGCTGATGGTCTTG	960							

Db	901	ACATAAGTAAAAAGACTTGTTCCTCCATTGCTTAAAGTCCACAGCATTTGTGTGATGCTCTTG	960
Qy	961	CCATTAACCTGAAAGATCTCTTTTAGACTGTACAGATCAATCTCTTAACAAATGCAACAA	1020
Db	961	CCATTAACCTGAAAGATCTCTTTTAGACTGTACAGATCAATCTCTTAACAAATGCAACAA	1020
Qy	1021	GAAGAAAGGGATTCTCTTTTTCACATCTGTCTTGACATCTGTCTTGCTCATGAGAATG	1080
Db	1021	GAAGAAAGGGATTCTCTTTTTCACATCTGTCTTGACATCTGTCTTGCTCATGAGAATG	1080
Qy	1081	ATATGAAGGAAGAGGTAGAAAGCAGATCTGTGTATAAAGAGACTTTAATGTGCTACTATGT	1140
Db	1081	ATATGAAGGAAGAGGTAGAAAGCAGATCTGTGTATAAAGAGACTTTAATGTGCTACTATGT	1140
Qy	1141	CATCTGTTCTTTTACATCTCTTGCTCTAGCTTATCTATCTATCAGTACATAGATCACT	1200
Db	1141	CATCTGTTCTTTTACATCTCTTGCTCTAGCTTATCTATCTATCAGTACATAGATCACT	1200
Qy	1201	TCTGTGTTCTCCAACAGTGAGGAAGATGCATCTTTTGAGTCTTTTAAACTTTACCTGCCGTT	1260
Db	1201	TCTGTGTTCTCCAACAGTGAGGAAGATGCATCTTTTGAGTCTTTTAAACTTTACCTGCCGTT	1260
Qy	1261	GGGAAATGGCATGGCTTCAGCAAGGACATCTCCATATGGAAGGCCGGTCAAACTTCA	1320
Db	1261	GGGAAATGGCATGGCTTCAGCAAGGACATCTCCATATGGAAGGCCGGTCAAACTTCA	1320
Qy	1321	GTTCTTAACAGATGTGTGATCTAGTCCACTCTTCTGAGAGCCCATTTTCTCTGTGTTCTC	1380
Db	1321	GTTCTTAACAGATGTGTGATCTAGTCCACTCTTCTGAGAGCCCATTTTCTCTGTGTTCTC	1380
Qy	1381	TTCTATAAATCGGATTTTCACTGTACTTGTATCTACTGCGCAAGTAGAACCTGCTCAGTA	1440
Db	1381	TTCTATAAATCGGATTTTCACTGTACTTGTATCTACTGCGCAAGTAGAACCTGCTCAGTA	1440
Qy	1441	GGTTCAAAAGTGAATTTTAAATAATTCATGTTTCAATTTTTCTGCTCAGGACTGCATT	1500
Db	1441	GGTTCAAAAGTGAATTTTAAATAATTCATGTTTCAATTTTTCTGCTCAGGACTGCATT	1500
Qy	1501	TATTCATGATATTTCTGTCATATATAGACCATGTTTCTTCCAGACAAAGCCCATAGGAAC	1560
Db	1501	TATTCATGATATTTCTGTCATATATAGACCATGTTTCTTCCAGACAAAGCCCATAGGAAC	1560
Qy	1561	TTTCCAGCAGCTCACACATTTGTAATAACATGTAATCTTTGAGTAGGAAAAATTAACATAA	1620
Db	1561	TTTCCAGCAGCTCACACATTTGTAATAACATGTAATCTTTGAGTAGGAAAAATTAACATAA	1620
Qy	1621	TAAATTAATTTGTCATATTTAGCAGCTCATTAAGAGCACTTCTATTAAGACTTTCTCAATC	1680
Db	1621	TAAATTAATTTGTCATATTTAGCAGCTCATTAAGAGCACTTCTATTAAGACTTTCTCAATC	1680
Qy	1681	TGATTTTGAAATTTGATAAACCCTTAATTTTAAATAACAAATATATCTTAACACCAACAT	1740
Db	1681	TGATTTTGAAATTTGATAAACCCTTAATTTTAAATAACAAATATATCTTAACACCAACAT	1740
Qy	1741	CTTCTCTTTTAAATAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	1800
Db	1741	CTTCTCTTTTAAATAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	1800
Qy	1801	ATGAACCCCATCT	1860
Db	1801	ATGAACCCCATCT	1860
Qy	1861	TCCCAATTTGATGCT	1920
Db	1861	TCCCAATTTGATGCT	1920
Qy	1921	ATGCACTTTGAGTATAGGCTTTCTACTGACCATAGCTCTCTCGGCAACCAATCCCATAC	1980
Db	1921	ATGCACTTTGAGTATAGGCTTTCTACTGACCATAGCTCTCTCGGCAACCAATCCCATAC	1980
Qy	1981	TCCACCTGCTCCAGCAGGGAACAATAGCAATTTGACCAATTTGACCAATTTGACGATGATTTT	2040
Db	1981	TCCACCTGCTCCAGCAGGGAACAATAGCAATTTGACCAATTTGACCAATTTGACGATGATTTT	2040

Db 592 GGGTCAGTGGCAATGGTGGACGGCACACTTTGACAAAGTCTCTGAGCTTCTGGGATGT 651
 Qy 624 TGGGAGCCCAACATATAGTATTTGGTGGAGGACTGTGCCACATAAGGACTCTTCAA 683
 Db 652 AGGGAGCCCAACATATAGTATTTGGTGGAGGACTGTGCCACATAGGAGACTCTTCAA 711
 Qy 684 CTCAGGAAGAACTGGAATGATAATCCCTGTTTCTACAGTATGCTTGGATTTGTGAGAT 743
 Db 712 CCCAAGGCCAAATTTGGAATGATGTAACTTCTTCTCAATATTTTCGGATTTTGGAAAT 771
 Qy 744 GCCAGAAATTAAGTCTCCAGGACTTAAGTGCAA-----GGAAATACAGGAGGACATGGCTTAC 798
 Db 772 GGTAGGAATAAATCTTTTGAACAAAGGAAATCTCTTTAAGAACAGAGGACCAACTCAA 831
 Qy 799 ATGCATGAAGAGAACAGAGTGAATGTATTAACAAACAAATCCACATAGAAATAAT 858
 Db 832 ATGTGTAAGAAGAGAGCAAGAACATGGCCACACCCGCCCCACACGAGAAATTTG 891
 Qy 859 CTATCAGGCATCAGAGGAGTGCACATGTATGTATTACTGGGACATAGTAAGAAAGACTT 918
 Db 892 TGGGCTGAACCTTCAAAGGACTTCTAAGTATTTTGTACTCTGATATAAATAAATAAGT 951
 Qy 919 GTTCCCATTTGCTAAAAGTCCACAGCATTTGCTGATGG-----TCTTGCCATTAACCTG 970
 Db 952 AGTTTAAATGTTATTAATTCATGTTACTGTGCTGAAGTGCAATTTCTCTCTAGCTTAGTCT 1011
 Qy 971 AAAGATCTCTTTTACAGTGTACAGATCAATTTCTTAACAAATGCACAAAGAAAGGG 1030
 Db 1012 CAGGTCTCTTCCAGAAATTTTCAAAAGCAATTCATACCTTTTGTGTACATTTGCGCTCATTT 1071
 Qy 1031 ATTCTCTTTTACATCTGTGTGACATCTGTCTTGTCTCATGAGAAATGATATGAAGA 1090
 Db 1072 TTTAGTGTTCGTATGAAGTACAGGACACAGGACCAAGAGAGTCTAGCAAGAGGG 1131
 Qy 1091 AGAGGTAGAAAGCAGATGTCTGTATAAGAGAGACTTTAAATGGTCACTATGTCTCTCTGTTTC 1150
 Db 1132 GATTTTGAAGGTGCGCTTCCAAAATCTCCTGAATCCGGGCTCTGTAGCAGGTCTCTTTC 1191
 Qy 1151 TTTCTACATCTTGGCTGTAGCTTATCTATCTATCTATCATAGTACATAGTCACTCTGTGTTCT 1210
 Db 1192 TTTCTAGCTTCTGACAGTCTGTCTTCTCTCTCTTCTGTTTTCATACCGTCTTCTATCTCTG 1251
 Qy 1211 CCA-----ACAGTGAGAGAGATGTCATCTTTGAGTCTT 1242
 Db 1252 CCAAGCATATATGCTCTTTACTCCCTGTATATGATGAAGAGCTTCTTCAAGTCAI 1311
 Qy 1243 TAAACTTACCTGCGCTTGGGAGAAATGGCATGGCTTT-----CAGCAAGGACA 1290
 Db 1312 GAAACTTA-TTCTGCTCAGATACCGGTGCGCTTTCTGGCTACAGGCTCCACTGCA 1370
 Qy 1291 TCTCATATGGAAGCCCGGTCAAACTTCAGTTCTCTTAACAGATGTGATGTAGTCCACTC 1350
 Db 1371 CTTCTTAGGAAGGAGTATGCGGACATAGCTTCCAAACAGGCTGTAAACAAAGTCCACCC 1430
 Qy 1351 -TTCTGAGGCCCATTTTCTGTTCTCTCTCTATTAAC-----TGGATTTCACTGTA 1405
 Db 1431 ATCCCTGGGGCTTCTTGTCTGCTCTTATTTTCAATTTGACTGAATGGATCTCACCAGAT 1490
 Qy 1406 CTGTATCTACTGCGCAAGTAGAACCTGTCTAGTAGTGTCAAAGTCAAAATTTATTTAAAAA 1465
 Db 1491 TTTGTATCTATTGCTCAGTAGAGACCGAGTCCAGTCCAAATAGTCAATTT-ATTCTAAGCGAACA 1549
 Qy 1466 TTCAATGTCACATTTTCTGCTCTCAGGAC 1494
 Db 1550 TTCAATGTCACATTTTCTGCTCTCAGGAC 1578

RESULT 3
 ID ADO24494
 AD ADO24494 standard; cDNA; 2143 BP.
 XX
 AC ADO24494;

XX 12-AUG-2004 (first entry)
 DT Human PRO244 encoding cDNA SEQ ID NO:133.
 DE human; PRO; antianaemic; antiarthritic; antiinflammatory; antipsoriatic;
 KW antirheumatic; dermatological; immunostimulant; immunosuppressive;
 KW osteopathic; vasotropic; immune related disease;
 KW inflammatory immune response; rheumatoid arthritis; osteoarthritis;
 KW juvenile chronic arthritis; systemic lupus erythematosus;
 KW spondyloarthritis; systemic sclerosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome;
 KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
 KW autoimmune disease; immune-mediated skin disease; bullous skin disease;
 KW erythema multiforme; contact dermatitis; psoriasis; lymphadenopathy;
 KW splenomegaly; leukopaenia; gene; ss.
 XX Homo sapiens.
 XX WO2004043397-A2.
 XX 27-MAY-2004.
 XX 12-NOV-2003; 2003WO-US036002.
 XX 12-NOV-2002; 2002US-0425931P.
 XX (GETH) GENENTECH INC.
 XX Abbas A, Bodary S, Clark H, Wu TD, Schoenfeld J, Wood WI;
 PI WPI: 2004-420080/39.
 DR P-PSDB; ADO24495.
 XX New isolated PRO polypeptide e.g. PRO37544, PRO69493, PRO87327 etc,
 PT capable of stimulating an immune response, useful for treating diseases
 PT such as rheumatoid arthritis, psoriasis, and leukopenia.
 PS Claim 2; SEQ ID NO 133; 326pp; English.
 CC The present invention describes an isolated human PRO polypeptide (I).
 CC Also described: (1) an isolated PRO nucleic (II) acid encoding (I); (2) a
 CC vector (III) comprising (II); (3) a host cell (IV) comprising (III); (4)
 CC producing (I); (5) a chimeric molecule (V) comprising (I) fused to a
 CC heterologous amino acid sequence; (6) an antibody (VI) which specifically
 CC binds to (I); (7) a composition of matter comprising (I), an agonist of
 CC (I), an antagonist of (I), or (VI) in combination with a carrier; (8)
 CC treating (M1) an immune related disorder in a mammal, by administering
 CC (I), an agonist of (I), an antagonist of (I), or the antibody (VI); (9)
 CC diagnosing an immune related disease in a mammal, by detecting the level
 CC of expression of a gene encoding (I) in a test sample of tissue cells
 CC obtained from the mammal and in a control sample of known normal tissue
 CC cells of the same cell type; (10) identifying a compound that inhibits the
 CC activity of (I); (11) identifying a compound (M2) that inhibits the
 CC expression of a gene encoding (I); (12) identifying a compound that
 CC mimics the activity of (I); and (12) stimulating the immune response in a
 CC mammal, by administering (I) or its antagonist to the mammal. (I) has
 CC antirheumatic, antiarthritic, antiinflammatory, antipsoriatic,
 CC antianaemic, dermatological, immunostimulant, immunosuppressive,
 CC osteopathic and vasotropic activities. (I) and (VI) are useful for
 CC diagnosing an immune related disease in a mammal. (II) is useful for
 CC diagnosing an inflammatory immune response in a mammal. (VI) is useful
 CC for determining the presence of (I) in a sample suspected of containing
 CC the polypeptide. (M1) is useful for treating a mammal having an immune
 CC related disorder chosen from rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, systemic lupus erythematosus,
 CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory
 CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
 CC autoimmune haemolytic anaemia, autoimmune or immune-mediated skin
 CC diseases including bullous skin diseases, erythema multiforme and contact
 CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
 CC present sequence encodes a human PRO protein from the present invention.
 XX

Example; Page 151; 173pp; English.

AAPF81741 to AAPF90177 encode the human membrane associated proteins
MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytosolic,
antiinflammatory, anticonvulsant, immunosuppressive, antiarrhythmic and
antiarteriosclerotic activities, which can be used in gene therapy.
MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
associated with decreased expression of functional MEMAP and antagonists
of MEMAP are used to treat a disease or condition associated with
overexpression of functional MEMAP. These disorders include cell
proliferative, autoimmune/inflammatory, neurological and gastrointestinal
disorders. The MEMAP polynucleotides and proteins are also useful for the
diagnosis of these disorders. Specific examples of these disorders
include cancer, inflammation, arteriosclerosis, epilepsy and diarrhoea.
MEMAP proteins can be used to screen for compounds which specifically
bind MEMAP including antibodies, oligonucleotides, proteins and small
molecules. MEMAP polynucleotides can be used to prepare transgenic
animals which can be studied to provide information concerning human
disease. Anti-MEMAP antibodies are useful in immunoassays for the
detection of MEMAP protein and can be used as antagonists to treat or
prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
can be delivered to target cells with genetic abnormalities with respect
to the expression of MEMAP to treat or prevent a disorder associated with

PS PS Sequence 968 BP; 314 A; 197 C; 205 G; 252 T; 0 U; 0 Other;
Query Match 17.5%; Score 441; DB 4; Length 968;
Best Local Similarity 73.0%; Pred. No. 1.8e-94;
Matches 611; Conservative 0; Mismatches 215; Indels 11; Gaps 3;

QY 87 AGAGGAAAGAAGGAAGCAGGGGCAATTTTCAAACCAACTCGCTGC 146
DB 125 AGAGGAGAGAAAACAACCAGAGAGAGAAAAAATAATTCTTAATCATCTGA 184
QY 147 ATCCACCACACAGAGAGAGTGCTTCAAAAACTCCCAGGTGCTCTCGGACGATAGC 206
DB 185 AACACATGCCAGAGAGAGATGCTTC---TCTTCCCAAAATGTTCTATGACTGTTGC 241
QY 207 CGGGGCTCATCTGTTTTCTAGTGCTGTTTCATCACAGATGTTGTHAACATATCG 266
DB 242 TGCGATCCCCATCTATTCTCAGTGCTGTTTCATCACAGATGTTGTCACATTCG 301
QY 267 CAGCTCTCAAA--TTTCCGGGAGAGACTTACAGCCACATAGAAATATTAAGSGCTTTC 323
DB 302 CATCTTTCAACCTGTGATGAGAAAAGTTTCAGCTACCTTGAGATTTACAGAGCTTC 361
QY 324 CTGCTACAGTGAGGCATCAGTTTCAGTCAAGAAATGCTGCTTCGAACTGGAACATTA 383
DB 362 CTGCTACAATATGATCAGTTTCAGTCAAGAAATGTTGTCATCACTGGAATATTT 421
QY 384 TCATCTAGTTGTTATTTTTCTTAGCAAACTTTCAGTCTGTCATCAAGTTTAAAGAA 443
DB 422 TCATCTAGTGCTGTTCTTTTCTACTGACCAATTTCTGCGCGTTAAAGTTTAAAGAA 481
QY 444 TTGCTCAGATCGGGGCTCACCTGCTGTTTATCGACACACAGAGAGCAGNATTCCT 503
DB 482 CTGCTCAGCATCGGGGCTCACCTGCTGTTTATCAACTCACAGAGAGCAGNATTCCT 541
QY 504 TTTTCGACAAAATCTAAAAGGAAAGTTTATATTTGAGCTCACAGACAGTGTTGA 563
DB 542 TTCCTACAGNAACCTAAATGAGAGATTTTTTATTTGACTGTGACACAGGTTGCGA 601
QY 564 GGFTCAGTGCAATGGGAGATGATACACTTTTTCAGAGTCCCTGACCTTCGGAATGC 623
DB 602 GGFTCAGTGCAATGGGAGATGATACACTTTTTCAGAGTCCCTGACCTTCGGAATGC 661
QY 624 TGGGAGCCCAACATATAGTTTTTGGTGGAGGAGCTGCCACCATAGGACTCTTCAA 683
DB 662 AGGGAGCCCAACATATAGTTTTTGGTGGAGGAGCTGCCACCATAGGACTCTTCAA 721
QY 684 CTCAGGAAGAACTGGAAATGATATCTCTGTTCTACAGTATGCCCTTGGATTGTGAGAT 743

246	Db	CATCTTTCAAACCTGTGATGAGAAAAGTTTTCAGCTACCTGAGAAATTTTCACAGAGCTCTC	303
324	Qy	CTGCTACAGTCAGGAGGAGGATCAGGTTTCAGTCAAGAAATTCGTCTCTTTGAACTGGAAACATTA	383
306	Db	CTGCTACAAATATGATCAGGTTTCAGTCAAGAAATTTGTTGCTCCATTGAACTGGGAATATTT	365
384	Qy	TCAATCTAGTTGTTATTTTCTCTACGACCACTTGACCTGGTCATCAAGTTTAAAGAA	443
366	Db	TCAATCCAGCTGCTACTTTCTTCTACTGACACCAATTTCTCTGGGCGTTAAGTTTAAAGAA	425
444	Qy	TTGCTTCAGACATGGGGGCTCACCTCGTGGTTATCGACACACAGGAGAGCAGGAATTCCT	503
426	Db	CTGCTACCCATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGACGAGAAATTCCT	485
504	Qy	TTTTTCGCAAAATCTAAAGGAAAGAGTTTTATATTTGGACTGCACAGACGAGTGGTGA	563
486	Db	TTCTCTACAAGAAACCTAAATCGAGAGAGTTTTTTTATTTGGACTGTCCAGACCAGGTTGTCCA	545
564	Qy	GGGTTCAGTGGCNAATGGGAGGATGATACACCTTTTCACAGAGTCCCTGACCTTCTGGGATGC	623
546	Db	GGGTTCAGTGGCAATGGGTGGACGGCACACCTTTTGACAAAGTCTCTGAGCTTCTGGGATGT	605
624	Qy	TGGGGAGCCCAACATATAGTTTGGTGGAGGACTGTGCCACCATAAAGGAGCTCTTCAAA	683
606	Db	AGGGAGGCCCAACCAATAGCTACCTTGGGAGGACTGTGCCACCATGAGAGACTCTTTCAA	665
684	Qy	CTCCAGGAAGAACTGGAATGATAAATCCCTGTTTTCACAGTATGCGCTTGGATTTGTGAGAT	743
666	Db	CCCAAGGCAAAATTGGATGATGAACCTGTTTCCCTCAATTTTCGGATTTGTGAAT	725
744	Qy	GCCAGAAATAAGTCTCTCAGGACTTAAGTGCA-----GGAAATACAAGGGACATGCGCTTAC	798
726	Db	GGTAGGAATAATCTTTGAAACAAAGGAAAAATCTCTTTAAGAACAGAGGCCACAACTCAA	785
799	Qy	ATGCATGAAGAAGACAAGAGTGATGTATTAACAACCAAAATCCACATAGAAAATAT	858
786	Db	ATGTGTAAGAAGGAGGAGCAAGAACATGGCCACACCCACCCGCCACACGAGAAATTTG	845
859	Qy	CTATCAGGCATCAGAAAGGACTGCACATGTATCTATTACTTGGGACATAAGTAAAGAA	915
846	Db	TGGCGTGAACCTCAAGGACCTCATAGTATTTGTTACTCTGATCAATAAANAATA	902
RESULT 8			
ADC78688			
ID	ADC78688	standard; cDNA; 997 BP.	
XX	ADC78688;		
AC	ADC78688;		
XX			
DT	01-JAN-2004	(first entry)	
XX			
DE	Human PRO244	cDNA.	
XX			
KW	antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;		
KW	nootropic; neuroprotective; vasotropic; chemotactic; angiogenic;		
KW	neurotrophic; osteopathic; antiaesthetic; antiaesthetic; antirheumatic;		
KW	antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;		
KW	thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;		
KW	gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;		
KW	Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;		
KW	nerve repair; thrombosis; bone; cartilage formation; angiogenesis;		
KW	asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;		
KW	atherosclerosis; cardiac injury; infertility; premature aging; AIDS;		
KW	diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.		
OS	Homo sapiens.		
XX			
PN	WO200015796-A2.		
XX			
XX			
PD	23-MAR-2000.		
XX			
PF	15-SEP-1999;	99WO-US021090.	
XX			

Db 606 AGGGAGGCCCAACAACATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTTTCAA 665
 Qy 684 CTCAGGAAGAAGTGAATGATATCCCTGTTTCTACAGTATGCCCTGTGATTTGTGAGAT 743
 Db 666 CCCAAGGCAAAATGGAATGATGTAACCTGTTTCTCTCAATTTTTCGGATTGTGAAT 725
 Qy 744 GCAGAAATTAAGTCTCTCAGGACTTAAGTGCA-----GGAAATACAAGGACATGGCTTAC 798
 Db 726 GGTAGAATTAATCTTTGACAAAGGAAATCTCTTTAAGAACAGAGGCACAATCTCA 785
 Qy 799 ATGTCATGAAGAAGAACAAGAGTGAATGATTAATAACAACCAAAATCCAACATAAGAAAAATAT 858
 Db 786 ATGTGTAAAGGAAGCAAGACATGCCACACCCACCCGCCACACGAGAAATTTG 845
 Qy 859 CTATCAGGCATCAGAAGGACTGCACATGATGATTTACTGGGACATAGTAAAGAGA 915
 Db 846 TCGCTGAACCTTCAAAGGACTTCAATAGTATTTGTTACTCTGTATACAAATAAAAAATA 902

RESULT 11

ID ACA60316 standard; cDNA; 997 BP.

AC ACA60316;

DT 12-JUN-2003 (first entry)

DE Human cDNA for secreted/transmembrane protein PRO244.

KW Human; ss; gene; secreted protein; transmembrane protein; PRO;

KW gene therapy; chromosome identification; chromosome marker.

XX Homo sapiens.

XX US2003003530-A1.

XX 02-JAN-2003.

PF 11-JUL-2001; 2001US-00904011.

XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 15-OCT-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 21-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063341P.

PR 28-OCT-1997; 97US-0063342P.

PR 28-OCT-1997; 97US-0063344P.

PR 28-OCT-1997; 97US-0063349P.

PR 28-OCT-1997; 97US-0063350P.

PR 28-OCT-1997; 97US-0063356P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US020594.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

WPI: 2003-329602/31.

P-PSDB; ABU71950.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing.

Claim 2; Fig 121; 484pp; English.

The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a PRO protein extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity to: (


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Db      69  AGAGAGAGAGAAACAAAAAACAAGAGAGAGAAAAATGAATTCATCTAAATCATCTGA 128
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RESULT 13
ID ACA73396 standard; cDNA; 997 BP.
XX
AC ACA73396;
XX
DT 01-JUL-2003 (first entry)
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DE Human secreted/transmembrane protein (PRO) cDNA #12.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003036146-A1.
XX
```

(GETH) GENENTECH INC.

PR	25-AUG-1999;	99US-00380142.	CC	PRO nucleotide sequences. The nucleotide sequences are useful as probes,
PR	01-SEP-1999;	99WO-US021011.	CC	in chromosome and gene mapping, in generating antisense RNA and DNA, in
PR	15-SEP-1999;	99WO-US021030.	CC	preparing PRO polypeptides by recombinant techniques and in gene therapy
PR	18-OCT-1999;	99US-00403297.	CC	(e.g. for replacement of defective gene). The PRO polypeptides are useful
PR	12-NOV-1999;	99US-00423844.	CC	as molecular weight markers for protein electrophoresis purposes, for
PR	01-DEC-1999;	99WO-US028301.	CC	chromosome identification, as chromosome markers, as therapeutic agents,
PR	02-DEC-1999;	99WO-US028551.	CC	for stimulating the release of TNF-alpha from human blood, for
PR	30-DEC-1999;	99WO-US031274.	CC	stimulating the proliferation or differentiation of chondrocytes and
PR	05-JAN-2000;	2000WO-US000219.	CC	detecting the presence of a tumour. The PRO polypeptides and nucleic
PR	18-FEB-2000;	2000WO-US004341.	CC	acids may also be used diagnostically for tissue typing. The sequences
PR	18-FEB-2000;	2000WO-US004342.	CC	presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
PR	22-FEB-2000;	2000WO-US004414.	CC	polypeptides of the invention
PR	24-FEB-2000;	2000WO-US005004.	XX	
PR	01-MAR-2000;	2000WO-US005601.	SQ	Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;
PR	02-MAR-2000;	2000WO-US005841.		
PR	15-MAR-2000;	2000WO-US006884.		
PR	30-MAR-2000;	2000WO-US008439.		
PR	17-MAY-2000;	2000WO-US013705.		
PR	22-MAY-2000;	2000WO-US014042.		
PR	30-MAY-2000;	2000WO-US014941.		
PR	02-JUN-2000;	2000WO-US015264.		
PR	28-JUL-2000;	2000WO-US020710.		
PR	22-AUG-2000;	2000US-00644848.		
PR	24-AUG-2000;	2000WO-US023328.		
PR	18-SEP-2000;	2000US-00664610.		
PR	18-SEP-2000;	2000US-00665350.		
PR	08-NOV-2000;	2000US-00709238.		
PR	08-NOV-2000;	2000WO-US030952.		
PR	01-DEC-2000;	2000WO-US032678.		
PR	20-DEC-2000;	2000US-00747259.		
PR	20-DEC-2000;	2000WO-US034956.		
PR	28-DEC-2001;	2001WO-US006520.		
PR	22-MAY-2001;	2001US-00816744.		
PR	10-MAY-2001;	2001US-00854208.		
PR	10-MAY-2001;	2001US-00854280.		
PR	25-MAY-2001;	2001US-00866028.		
PR	01-JUN-2001;	2001WO-US017800.		
PR	05-JUN-2001;	2001US-00874503.		
PR	20-JUN-2001;	2001WO-US019692.		
PR	29-JUN-2001;	2001WO-US021066.		
PR	09-JUL-2001;	2001WO-US021735.		
PR	18-JUL-2001;	2001US-00908827.		
PR	30-JUL-2001;	2001US-00918585.		
PR	06-AUG-2001;	2001US-00924419.		
PR	13-AUG-2001;	2001US-00929404.		
PR	16-AUG-2001;	2001US-00931836.		
PR	28-AUG-2001;	2001US-00941992.		
PR	29-AUG-2001;	2001US-00942099.		
PR	04-SEP-2001;	2001WO-US027099.		
PR	15-JAN-2002;	2002US-00052586.		
PA	(GETH) GENENTECH INC.			
XX				
XX				
PI	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;			
PI	Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;			
XX				
XX	WPI; 2003-332039/31.			
DR	P-PSDB; ABU67417.			
XX				
XX				
PT	New secreted and transmembrane PRO polypeptides and nucleic acids, useful			
PT	in gene therapy, in chromosome and gene mapping, as chromosome markers,			
PT	in tissue typing, and in chromosome identification.			
XX				
XX	Claim 2; Fig 23; 706pp; English.			
XX				
CC	The invention discloses human nucleic acids encoding secreted and			
CC	transmembrane (PRO) polypeptides. Also disclosed is an antibody that			
CC	specifically binds to the PRO polypeptide, a method for stimulating the			
CC	release of tumour necrosis factor alpha (TNF-alpha) from human blood by			
CC	contacting the blood a PRO polypeptide, a method for stimulating the			
CC	proliferation or differentiation of chondrocyte cells by contacting the			
CC	cells with a PRO polypeptide, a method for detecting the presence of a			
CC	tumour in a mammal and an oligonucleotide probe derived from any of the			

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2005, 03:48:21 ; Search time 8065 Seconds
(without alignments)
11879.450 Million cell updates/sec

Title: US-10-812-620-1

Perfect score: 2517
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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EST.*

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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1991	79.1	2233	3 AK089286	AK089286 Mus muscu
2	1338	53.2	4017	3 AK036493	AK036493 Mus muscu
3	818.6	32.5	865	9 BX963867	BX963867 Reverse s
4	706.2	28.1	731	4 BG067349	BG067349 H3053D08-
5	696.6	27.7	756	6 B761232	B761232 B761232
6	665.6	26.4	705	6 B764212	B764212 B764212
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24	484.4	19.2	486	5 BX516799	BX516799 BX516799

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27	456.4	18.1	489	6 BY529779	BY529779 BY529779
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33	432	17.2	452	6 BY552321	BY552321 BY552321
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41	416	16.5	448	6 BY530505	BY530505 BY530505
42	415.4	16.5	438	6 BY537115	BY537115 BY537115
43	411	16.3	414	5 BY207927	BY207927 BY207927
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ALIGNMENTS

RESULT 1	AK089286	2233 bp	mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730001C01 product:C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, full insert sequence.	linear	HTC 03-APR-2004
LOCUS	AK089286				
DEFINITION	AK089286				
ACCESSION	AK089286				
VERSION	AK089286.1	GI:26105181			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
REFERENCE	5				

AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL REFERENCE
Nature 420, 563-573 (2002)

AUTHORS
6 (bases 1 to 2233)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haehizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers
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Db	1680	AATTAAACTAAATAAATAATTTGACATATATTAGCACTCATATAGAGCACTTCTATATTAGAC	1739
Qy	1669	TTTCTCACAATCTGATTTTCGAAATTGATACCTTATTTTAAATACAAATATATCTTACAA	1728
Db	1740	TTTCTCACAATCTGATTTTCGAAATTGATACCTTATTTTAAATACAAATATATCTTACAA	1799
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Db	1860	AATTCACTTTTAATGAACCCATCCTTACTCTCTCTACACAACTGCTCTATCCACCTC	1919
Qy	1849	ACTGATTTTCCCTCCCAATTTTCATGCTCCTCTTTGTTTAAACCACTCTATCTGCTC	1908
Db	1920	ACTGATTTTCCCTCCCAATTTTCATGCTCCTCTTTGTTTAAACCACTCTATCTGCTC	1979
Qy	1909	AGTGCTTCCTGAATGCACTTGAGTATAAGGCTTCTACTGGACCATAGCCTCTCGGCAAC	1968
Db	1980	AGTGCTTCCTGAATGCACTTGAGTATAAGGCTTCTACTGGAACCATAGCCTCTCGGCAAC	2039
Qy	1969	CACATCCCATCTCCACCTGCTCCAGCAGGGAACAATAGCCAAATGACCATCTTCAGCTG	2028
Db	2040	CACATCCCATCTCCACCTGCTCCAGCAGGGAACAATAGCCAAATGACCATCTTCAGCTG	2099
Qy	2029	AGGATGG- AATTTCATGAGCTCCATGCCATTCATGCTGGAATTTGGGTGTTTATGTAAAC	2087
Db	2100	AGGATGGAAATTTTCATGAGCTCCATGCCATTCATGCTGGAATTTGGGTGTTTATGTAAAC	2159
Qy	2088	CTTTATTATATTTGGTCTATCTCTTCTGTATCCCTAGAAATCTCTAGGAGCTTCATATTTAAA	2147
Db	2160	CTTTATTATATTTGGTCTATCTCTTCTGTATCCCTAGAAATCTCTAGGAGCTTCATATTTAAA	2219
Qy	2148	AGATTCTGAATTC	2161
Db	2220	AGATTCTGAATTC	2233
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AK036493			
LOCUS			
DEFINITION	AK036493 4017 bp mRNA linear HTC 03-APR-2004		
LOCUS	Mus musculus adult male bone cDNA, RIKEN full-length enriched		
DEFINITION	library, clone:9830118H07 product:C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, full insert sequence.		
AK036493			
ACCESSION	AK036493		

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	Matches 1369; Conservative 0; Mismatches 15;	
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QY	316	GAGCTTCTCTGCTACAGTCAGGATCAGGTTGAGTCAAGAAATGCTGCTTTGAACCTGG 375
DB	2692	GAGCTTCTCTGCTACAGTCAGGATCAGGTTGAGTCAAGAAATGCTGCTTTGAACCTGG 2751
QY	376	AAACATTATCAATCTAGTTGTTATTTTCTCTAGACAACTTGACCTGGTCATCAAGT 435
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QY	436	TTAAAGAAATTTGCTCAGACATGGGGCTCACCTGGTGGTTATCGACACACAGGAAGCAG 495
DB	2812	TTAAAGAAATTTGCTCAGACATGGGGCTCACCTGGTGGTTATCGACACACAGGAAGCAG 2871
QY	496	GAAATCTCTTTTCGCACAAATCTAAAGGAAAGATTTTATTTATTTGGACTGACAGACCG 555
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QY	556	GTGGTGGAGGGTCAGTGGCAATGGGAGGATGATACACCTTTTCACAGAGTCCCTGACCTTC 615
DB	2932	GTGGTGGAGGGTCAGTGGCAATGGGAGGATGATACACCTTTTCACAGAGTCCCTGACCTTC 2991
QY	616	TGGATGCTGGGAGCCCAACAATATAGTTTTGGTGGAGGACTGTGCCACCAATAGGGAC 675
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QY	676	TCTTCAAACTCCAGGAGAACTGGAATGATATCCCTGTTTCTACAGTATGCTTGGATT 735
DB	3052	TCTTCAAACTCCAGGAGAACTGGAATGATATACCCCTGTTTCTACAGTATGCTTGGATT 3111
QY	736	TGTGAGATGCCAGAATAAGTCTCAGGACTAAGTCAAGGAAATACAGGGACATGGCT 795
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DB	3532	TACATCTTGGCTCTAGCTTATCTATCTATCAGTACATAGATCACTTCTGTGTTCTCAA 3591
QY	1215	CAGTGAGAAAGATGCATCTTTGAGTCTTTAAACTTACCTGCGCTTGGGAGAAATGGCATG 1274
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DB	3712	GTGATCTAGTCCACTCTTCTGAGGCCCATTTTCTGTGTCTCTCTATATAAACTGGA 3771
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QY	1515	CTGCAATATAGACCATGTTTCTTCCAGACAAAGCCCATTAGGAA-CTTCAGCAGCAGTC 1573
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QY	1634	CATATT 1639
DB	4012	CATATT 4017
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LOCUS		
DEFINITION		
Reverse strand read from insert in 5'HPRT insertion targeting and		
chromosome engineering clone MHPN49e21, genomic survey sequence.		
BX963867		
ACCESSION		
BX963867.1 GI:49695290		
VERSION		
GSS; genome survey sequence; MICER.		
KEYWORDS		
Mus musculus (house mouse)		
SOURCE		
ORGANISM		
Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
1 (bases 1 to 865)		
REFERENCE		
AUTHORS		
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,		
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,		
Rogers,J. and Bradley,A.		
Direct Submission		
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,		
CB10 1SA, UK. http://www.sanger.ac.uk/MICER		
TITLE		
JOURNAL		
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source		
ORIGIN		

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QY	1397	TCACCTGTACTTGTATCTTACTCGGCAAGTAGAACCTGCTCAGTAGGTTCAAAGTGAATTT	1456		
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QY	1457	ATTTAAAAATTCATGTTTACATTTTCTGTCTCAGGACTGCATTTATGCAATGATATTTCT	1516		
DB	127	ATTTAAAAATTCATGTTTACATTTTCTGTCTCAGGACTGCATTTATGCAATGATATTTCT	186		
QY	1517	GTCAAATATAGACCATGTTTCTTCCAGACAAAGCCCATTTAGGAA-CTTCAGGAGCAGTCAC	1575		
DB	187	GTCAAATATAGACCATGTTTCTTCCAGACAAAGCCCTAAAGGAAACCTTTTCAGCAGCAGTCAC	246		
QY	1576	ACATTGTAATAACATGATCTTCTTGGAGTAGGAAAAATTAACCTAAATAAATTAATTTGTCA	1635		
DB	247	ACATTGTAATAACATGATCTTCTTGGAGTAGGAAAAATTAACCTAAATAAATTAATTTGTCA	306		
QY	1636	TATTAGCACTCATTTACGAGCACTTCTTATTAGACTTTTCTCAAACTCTGATTTTGAAATTTGA	1695		
DB	307	TATTAGCACTCATTTACGAGCACTTCTTATTAGACTTTTCTCAAACTCTGATTTTGAAATTTGA	366		
QY	1696	TAACTTATTTTAAAAATACAAATATATCTTACACACACATTTGCACTTCTCTTTTAAAA	1755		
DB	367	TAACTTATTTTAAAAATACAAATATATCTTACACACACATTTGCACTTCTCTTTTAAAA	426		
QY	1756	TTATTTTGTGTTTGAATAATTTTGTGCATTTATATAATTAATTAATTAATTAATTAATTA	1815		
DB	427	TTATTTTGTGTTTGAATAATTTTGTGCATTTATATAATTAATTAATTAATTAATTAATTA	486		
QY	1816	CTCTCTCTCACTACAACTGCTCTCTATCCACTCACTGATTTTCCCTCCCAATTTTCATGTG	1875		
DB	487	CTCTCTCTCACTACAACTGCTCTCTATCCACTCACTGATTTTCCCTCCCAATTTTCATGTG	546		
QY	1876	CTCTCTTTGTTTAAACCCCACTCTATCTGCTCAGTGTCTTCCCTGAAATGCACTTTGAGTATA	1935		
DB	547	CTCTCTTTGTTTAAACCCCACTCTATCTGCTCAGTGTCTTCCCTGAAATGCACTTTGAGTATA	606		
QY	1936	AGGCTTTCTACTGGACCATAGCCTCTCGGCAACACATCCCATCTCCACTGCTCCAGC	1995		
DB	607	AGGCTTTCTACTGGACCATAGCCTCTCGGCAACACATCCCATCTCCACTGCTCCAGC	666		
QY	1996	AGGGAACAATAGCCAATTTGACCATCTTTCAGCTGAGGATGG-ATTTTCATGAGCTCCATGCC	2054		
DB	667	AGGGAACAATAGCCAATTTGACCATCTTTCAGCTGAGGATGGAAATTTTCATGAGCTCCATGCC	726		
QY	2055	ATTTCATGCTGGAATTTGGGTGTGTTTATGTAACCTTTATTAATATGTTGCTATCTCTTCTG	2114		
DB	727	ATTTCATGCTGGAATTTGGGTGTGTTTATGTAACCTTTATTAATATGTTGCTATCTCTTCTG	786		
QY	2115	TATCCCTAGAAATCTCTAGGAGCTTCATATTAAGAAATTTCTGAATTCATCAAAAGGGCACA	2174		
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QY	2175	CAAGAATAACCAAAAGACC 2193			
DB	847	CAAGAATAACCAAAAGACC 865			

RESULT 4
BG067349/c
LOCUS
DEFINITION H3053D08-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
ACCESSION BG067349
VERSION BG067349.2 GI:40014147

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
EST.
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheraia; Chordata; Vertebrata; Euteleostomi;
Eukaryota; Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 731)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
20381348
10922068
On Jan 26, 2001 this sequence version replaced gi:12549918.
Other ESTs: H3053D08-5
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgaun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit <http://lgaun.grc.nia.nih.gov/cDNA/15k.html> for details.
Plate: H3053 row: D column: 08
Seq primer: -21M13 Forward
High quality sequence stop: 731
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/lab_host="DH10B"
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/notes="Vector: pSPORT1; Site_1: SalI, Site_2: NotI; This
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embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5
embryos, and E12.5 female mesonephros/gonad) and one
newborn ovary cDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dT)-Not primers. References include: (1)
Genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse developmental
cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A., 97:
9127-9132; (2) Large-scale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
development, 2000, Development, 127: 1737-1749; (3)
Genome-wide mapping of unselected transcripts from
extraembryonic tissue of 7.5-day mouse embryos reveals
enrichment in the t-complex and under-representation on
the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN

Query Match		28.1%;	Score 706.2;	DB 4;	Length 731;
Best Local Similarity		98.8%;	Pred. No. 2.6e-160;		
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Qy	970	GAAAGATCTCTTTTATAGACTGTACAGATCAATTTCTTAACAAATGCACAGAGAAGG	1029		
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Db 7 CTCTCTTTTAAATATTTTG-TTGAAATNNNTGTCATATATAAATTCACCTTTTAATG 65
Qy 1804 AACCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1863
Db 66 AANCCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125
Qy 1864 CAATTCATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1923
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Qy 1924 CACTTGAGTAAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1983
Db 186 CACTTGAGTAAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 245
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RESULT 6
BY764212 705 bp mRNA linear EST 17-DEC-2002
LOCUS BY764212 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
DEFINITION cells Mus musculus cDNA clone F730001C01 3', mRNA sequence.
ACCESSION BY764212
VERSION BY764212.1 GI:27201526
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 705)
REFERENCES
Ozaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yananaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Bruscia, V.,
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawai, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pertes, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. D., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
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Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wynehaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Waki, K., Kawai, J., Aizawa, K.,
Akakawa, T., Fukuda, S., Hara, A., Haseizume, W., Imotani, K., Iehi, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, B. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12468851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resseq@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-Format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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BY763813 GI:27200881

ACCESSION

BY763813

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Guatini, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltas, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pebole, G.,
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JOURNAL
MEDLINE
PUBMED

COMMENT

22354683

12466851

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Direct Submission

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Location/Qualifiers

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/strain="NOD"

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/clones="F630012G18"

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DEFINITION	BY747821 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630011J05 5', mRNA sequence.							
ACCESSION	BY747821							
VERSION	BY747821.1	GI:27176312						
KEYWORDS	EST.							
SOURCE	Mus musculus (house mouse)							
ORGANISM	Mus musculus							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 666)							
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batolov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Santelina, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sundelin, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.							
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JOURNAL	Nature	420	563-573	(2002)				
MEDLINE	22354683							
PUBMED	12466851							
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/ Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken							

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RESULT 12
BY749084
LOCUS
DEFINITION
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dendritic cells Mus musculus cDNA clone F630224E05 5', mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Matches 649; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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ACCESSION
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VERSION
BG080418.2 GI:40014148
KEYWORDS
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ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 644)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Doi,H.,
Grabovac,M.J., Pantano,S., Sano,Y., Piao,Y., Negaraja,R., Wood,W.H.
III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
20381348
10922068
On Jan 26, 2001 this sequence version replaced gi:12562986.
Other ESTs: H3053D08-3
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3053 row: D column: 08
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clone is among a rearranged set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5
embryos, and E12.5 female mesonephros/gonad) and one
newborn ovary cDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dT)-Not primers. References include: (1)
Genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse developmental
cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97:
9127-9132; (2) Large-scale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
development, 2000, Development, 127: 1737-1749; (3)
Genome-wide mapping of unselected transcripts from
extraembryonic tissue of 7.5-day mouse embryos reveals
enrichment in the t-complex and under-representation on
the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
ORIGIN
Query Match 25.0%; Score 628.2; DB 4; Length 644;
Best Local Similarity 99.4%; Pred. No. 2.3e-141;
Matches 641; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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RESULT 14
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LOCUS
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musculus cDNA clone I830011F16 5', mRNA sequence.
ACCESSION
BY743467
VERSION
BY743467.1 GI:27169524
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 645)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamana,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojibori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kenapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V.,
Chotha,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
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Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, C., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wyehaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12456851
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, P.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry
and Microbiology/Parasitology Institute for Molecular Bioscience
University of Queensland Brisbane, Q 4072 Australia) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES

Location/Qualifiers
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Job time : 8079 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2005, 13:17:52 ; Search time 185 Seconds
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Title: US-10-812-620-2

Perfect score: 1179

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	774	65.6	997	4	US-09-905-125A-376
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5	774	65.6	997	4	US-09-903-603A-376
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7	774	65.6	997	4	US-09-909-064-376
8	774	65.6	997	4	US-09-905-381A-376
9	774	65.6	997	4	US-09-906-618-376
10	392.5	33.3	1227	3	US-08-772-440-3
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12	336	28.5	501	3	US-08-772-440-20

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c 22	310	26.3	301	4	US-09-433-826B-29	Sequence 29, Appl
c 23	310	26.3	301	4	US-09-604-287A-29	Sequence 29, Appl
c 24	310	26.3	301	4	US-09-285-480-29	Sequence 29, Appl
c 25	310	26.3	301	4	US-09-834-759-29	Sequence 29, Appl
c 26	310	26.3	301	4	US-09-590-751A-29	Sequence 29, Appl
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c 43	235.5	20.0	1277	4	US-09-016-434-1186	Sequence 1186, Ap
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ALIGNMENTS

RESULT 1

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; Sequence 376, Application US/09907794A

; Patent No. 8635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

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; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR FILING DATE: 2000-01-05
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; ORGANISM: Homo Sapien
US-09-907-794A-376

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Best Local Similarity: 66.51% Mismatches: 43
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US-10-812-620-2 (1-214) x US-09-907-794A-376 (1-997)

QY 1 MetAsnSerThrLysSerProLaserHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerClyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTCTCTGGATCCCATCTTATTTCTCAGTGCCTGTGTTATC 222
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTTCCATCTTTCAAACTGTGATGAGAAAAAGTTTCAGCTA 282
QY 60 HisArgAsnIleGlyLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAATTTACAGAGCTCTCTGCTACAAATTATGGATCAGGTTCAAGCAAGATTGT 342
QY 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAATCGGAATATTTCAATCCAGTCTACTTCTTTCTACTGACACCACT 402
QY 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValLilleAsp 119
Db 403 TCTTGGCGCTTAAGTTTAAGAACTGCTCAGCCATGGGGGCTCCTCTGTGTGTTATCAAC 462
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QY 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGGAATTCCTTTCTTACAGAAACCTAAATCAGAGAGTTTTTATT 522
QY 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTTCAGACCAAGTTGTCGAGGTCAGTGGCAATGGTGGACGGCACACCTTTTGACA 582
QY 160 GluSerLeuSerPheTrpAspAlaGlyClnProAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGGCCCAACAACATAGCTTACCTGGAGGACTGT 642
QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACATGAGAGACTCTTCAACCCCAAGGCAAAATGGAATGATGTAACTGTTTCTC 702
QY 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGATTTGTGAAATGTTAGGAATAAATCCTTTTGAAC 747

RESULT 2
US-09-905-125A-376
; Sequence 376, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
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;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 376
;; LENGTH: 997
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-905-125A-376

Alignment Scores:
Pred. No.: 7,27e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 4 Gaps: 2

US-10-812-620-2 (1-214) x US-09-905-125A-376 (1-997)

Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATCATCATTAATCATCTGAAACACAAATGCACAGAGAGATGCTTC---TCCTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPhele 40
Db 163 CAATGTCTTATGGAGCTGTGCTGGATCCCATCTATTCTTCAGTGCCTGTTTCA 222
Qy 41 ThrArgCysValValThrTrpArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTCCGATCTTTCAAACCTGTGTATGAGAAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAAATTTTCACAGAGCTCTCTGCTACAAATTTATGGATCAGGTTTCAGTCAAGAAATGT 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 343 TGTCTATGAACTGGGAATATTTCAATCCAGCTGCTACTTCTTTCTACTGACCACTT 402
Qy 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 403 TCCTGGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrlle 139
Db 463 TCACAGGAGGAGCAGGAATTCCTTTCTCTACAGAAACCTAAATGAGAGAGTTTTTTAT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGATCTGTACAGACCAAGTTTGTGAGGGTCAGTGGCAATGGGTGGAGCGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTCGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTy 199
Db 643 GCCACCAATGAGAGACTCTTCAAAACCCCAAGGCAAAATTTGGAATGATGTAAACCTGTTTCCTC 702

Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGGATTTCGAAATGCTAGGAATAAATCCTTTGAAC 747

RESULT 3

US-09-902-775A-376
;; Sequence 376, Application US/09902775A
;; Patent No. 6686451
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, A.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/902,775A
;; PRIOR FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20

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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-775A-376

Alignment Scores:
Pred. No.: 7,27e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: Gaps: 2

US-10-812-620-2 (1-214) x US-09-902-775A-376 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGATTCATCTAATCATCTGAAACACATCGACAGAGAGGATGCTTC---TCTTCC 162

Qy 21 GlnValLeuSerThrPheLeuAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGATCCCATCTATTCTCAGTGCCTGTTTTCATC 222

Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTTTCGCATCTTTCAACCTGTGATGAGAAAAGTTTCAGCTA 282

Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAATTTTCACAGAGCTCTCTGCTACAAATATGATCAGGTTCAGTCAAGATTGT 342

Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATGAACTGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAT 402

Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValLilleAsp 119
Db 403 TCTTGGCGGTTAAGTTTAAAGAACTGCTCAGGCATGGGGGCTCACCCTGGTGTATCAAC 462

Qy 120 ThrGlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACAGGAATCTCTTCTACAGAAACCTAAATAGAGAGTATTTTATT 522

Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTACAGACAGGTTGTCAGGGTCAAGTGGCAATGGTGGACGGCACACCTTTGACA 582

Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTGTAGGTTCTGGGATGTAGGGGAGCCCAACATAGCTACCTGGAGGAGCTGT 642

Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACATGAGAGACTCTTCAAAACCAAGCAAAATGGAAATGATGATACCTGTTTCCTC 702

Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGGATTGTGAAATGGTAGGAATAAATCCTTTTGAAC 747

RESULT 4
US-09-906-700-376
; Sequence 376, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
```

```
Alignment Scores:
Pred. No.: 7,27e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: Gaps: 2
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US-10-812-620-2 (1-214) x US-09-906-700-376 (1-997)
Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTCATCTAAATCATCTGAACACAACTGCACAGAGAGGATGCTTC--TCTTCC 162
Qy 21 GlnValLeuSerThrThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAATATGTTCTTATGGACTGTTGCTGGGATCCCATCTCTATTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATCTTCGATCTTTCAACCTGTGATGAGAAAGATTTCAGCTA 282
Qy 60 HisArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
Db 283 CCTGAGAATTTTCACAGAGCTCTCTGCTACAAATATGATGATCAGGTTTCAGTCAAGATGTT 342
Qy 80 CysProLeuAenThrLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTTGAATCGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCATTT 402
Qy 100 ThrTrpSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 403 TCCTGGGGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGCTCACCCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACGAGGAATTCCTTCTTACAGAAACCTTAAATGAGAGAGTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTGACAGACCAAGTTGTCAGGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAenIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGACTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAenTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATGGGAATGATGTAACCTGTTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGGATTTGTGAATGCTAGGAATAAATCTTTGAAC 747

RESULT 5
US-09-903-603A-376
; Sequence 376, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
```

```
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903.603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-603A-376

Alignment Scores:
Pred. No.: 7,27e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservations: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 4 Gaps: 2

US-10-812-620-2 (1-214) x US-09-903-603A-376 (1-997)
Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTCATCTAAATCATCTGAACACAACTGCACAGAGAGGATGCTTC--TCTTCC 162
Qy 21 GlnValLeuSerThrThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAATATGTTCTTATGGACTGTTGCTGGGATCCCATCTCTATTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATCTTCGATCTTTCAACCTGTGATGAGAAAGATTTCAGCTA 282
Qy 60 HisArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
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Db 283 CCTGAGAAATTTACAGAGCTCTCTCTACAAATATTGGATCAGGTTCAAGAAATGT 342
Qy 80 CysProLeuAsnTrpLysHisItyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAATCGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACCAAT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValleAsp 119
Db 403 TCTCGGGCTTAAGTTTAAAGACTGCTCAGCCATGGGGCTCACTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACGAGAAATTCCTTCTCAAGAAACCTAAATGAGAGAGTTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThr 159
Db 523 GCACTGTCTACAGCAGGTTGTGAGGGTCACTGGCAATGGTGGCGCACACCTTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AGTCTCTGAGCTTCTGGAGTAGGGGAGCCCAACATAGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATTTGGAATGATGTAACCTGTTTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGAGTTTGTGAATGTTAGGAATAAATCCTTTGAAC 747

RESULT 6

US-09-904-920A-376

; Sequence 376, Application US/09904920A

; Patent No. 6806352

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/904,920A

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-920A-376

Alignment Scores:

Pred. No.:	7,27e-88	Length:	997
Score:	774.00	Matches:	143
Percent Similarity:	79.07%	Conservative:	27
Best Local Similarity:	66.51%	Mismatches:	43
Query Match:	65.65%	Indels:	2
DB:	4	Gaps:	2

US-10-812-620-2 (1-214) x US-09-904-920A-376 (1-997)

Qy	1	MetAsnSerThrLysSerProAlaSerHisIthrGluArgGlyCysPheLysAsnSer	20
Db	106	ATGAATTCATCTAATCATCTGAAACAAATGCACAGAGAGGATGCTTC---TCTTCC	162
Qy	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
Db	163	CAAAATGTTCTTATGGACTGTTGCTGGGATCCCATCTTATTTCTCAGTGCCTGTTTCATC	222
Qy	41	ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro	59
Db	223	ACCAGATGTGTTGTGACATTTTCGTCATCTTTCAAAACCTGTGATGAGAAAAAGTTTCAGCTA	282
Qy	60	HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys	79
Db	283	CCTGAGAAATTTCAACAGAGCTCTCTCTGTCACAAATATGATCAGTTCAAGAAATGT	342
Qy	80	CysProLeuAsnTrpLysHisIthrGlnSerSerCysTyrPhePheSerThrThrLeu	99
Db	343	TGTCCATTGAATCGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACCACTT	402
Qy	100	ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValleAsp	119
Db	403	TCCTGGGCGTTAAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC	462
Qy	120	ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle	139
Db	463	TCACAGGAGGAGCAGGAATTCCTTCTCAAGAAACCTAAATGAGAGAGTTTTTATT	522
Qy	140	GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThr	159

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mathet, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906.618
CURRENT FILING DATE: 2001-07-16
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: US 60/143,048
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145,698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: US 60/146,222
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/20594
PRIORITY FILING DATE: 1999-09-08
PRIORITY APPLICATION NUMBER: PCT/US99/20944
PRIORITY FILING DATE: 1999-09-13
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/21547
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/23089
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: PCT/US99/28214
PRIORITY FILING DATE: 1999-11-29
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: 1999-11-30
PRIORITY APPLICATION NUMBER: PCT/US99/28564
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/28565
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIORITY FILING DATE: 1999-12-16
PRIORITY APPLICATION NUMBER: PCT/US99/30911
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
PRIORITY FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
LENGTH: 997
TYPE: DNA
ORGANISM: Homo Sapien
US-09-906-618-376

Alignment Scores:
Pred. No.: 7,27e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 4 Gaps: 2

US-10-812-620-2 (1-214) x US-09-906-618-376 (1-997)

Qy 1 MetAenSerThrTrpAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTCATCTAATCATCTTGAACACAAATGACAGAGAGGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40

Db 163 CAAATGTTCTTATGGACTGTGTGGGATCCCCATCTATTTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTrpArgSerSerGlnIleSerGlyGln---AenLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTTCCGATCTTTCAACCTGTGTATGAGAAAAGTTTCAGGTA 282
Qy 60 HisArgAenIleLysGluLeuSerCysTrpSerGluAlaSerGlySerValLysAenCys 79
Db 283 CCTGAGAATTTTCACAGAGCTCTCTCTGCTACAAATATATGATCAGGTTTCAGTCAAGAAATTGT 342
Qy 80 CysProLeuAenTrpLysHisTrpGlnSerSerCysTrpPhePheSerThrThrLeu 99
Db 343 TGTCATTTGAACCTGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAATT 402
Qy 100 ThrTrpSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAep 119
Db 403 TCCTGGCGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGCTCACCCTGGTGTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysProLysArgLysGluPheTrpIle 139
Db 463 TCACAGGAGGAGCAGGAATTCCTTCTCTACAGAAACCTAAATGAGAGAGATTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTACAGCAGGTTGTCAGGGTTCAGTGGCAATGGGTGGACGGCACACCTTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGCCCAACAAATAGCTACCTCGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAenTrpAenAspIleProCysPheTrp 199
Db 643 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATTTGGAATGATGTAACCTGTTTCCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAep 214
Db 703 AATTATTTTCGGATTTGTGAATGGTAGGAATAAATCCTTTGAAC 747

RESULT 10
US-08-772-440-3
Sequence 3, Application US/08772440
Patent No. 6046158
GENERAL INFORMATION:
APPLICANT: Arizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HERewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577

;; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
;; TITLE OF INVENTION: THEREOF
;; NUMBER OF SEQUENCES: 42
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77210
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/772,440
;; FILING DATE: CONCURRENTLY HERewith
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parker, David L.
;; REGISTRATION NUMBER: 32,165
;; REFERENCE/DOCKET NUMBER: UTXD:493
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 512/418-3000
;; TELEFAX: 512/474-7577
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 501 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-772-440-20

Alignment Scores:
Pred. No.: 6.66e-33 Length: 501
Score: 336.00 Matches: 67
Percent Similarity: 58.90% Conservative: 29
Best Local Similarity: 41.10% Mismatches: 55
Query Match: 28.50% Indels: 12
DB: 3 Gaps: 3

US-10-812-620-2 (1-214) x US-08-772-440-20 (1-501)

Qy 58 GlnProHisArgAsnIleLysGlu-----LeuSerCysTyrSer 70
Db 13 CAGCCAGTAGACACTATATGAACCTTCACATACCATCCAGTCTCAGCTGCTCAGT 72

Qy 71 Glu-----AlaSerGlySerValIleAsnCysCysProLeuAsnTrpLysHisTyr 87
Db 73 GAAGGGACTATGGTGTGAGAAAAATGTGGGATGCTGCCAAATCACTGGAAGTCAATT 132

Qy 88 GlnSerSerCysTyrPhePheSerThrThrLeuThrTrpSerSerSerLeuLysAsn 107
Db 133 GGCTCCAGCTGCTACCTATTCTACCAAGAGAACTTCTGGAGCACCAGTGAGCAGAAC 192

Qy 108 CysSerAspMetGlyAlaHisLeuValValIleAspThrGlnGluGlnGluPheLeu 127
Db 193 TGTGTTTCAGATGGGGGCTCATCTGTGTGATCATCTGAAGCGGAGCAGAAATTCATC 252

Qy 128 PheArgThrLysProLysArgLysGluPheTyrIleGlyLeuThrAspGlnValValGlu 147
Db 253 ACCCAGCAGCTGAATGATCACTTTCTTACTTCCTGGGTCTTTCCGATCCACAGGTAAT 312

Qy 148 GlyGlnTrpGlnTrpValAspAspThrProPheThrGluSerLeuSerPheTrpAspAla 167
Db 313 GGCAATGGCAATGGATCGATGATCTCTTTCAGTCAAAATGTGAGTTCTGTCACCCC 372

Qy 168 GlyGluProAsnAsnIleValLeuValGluAspCysAlaThrIleArgAspSerSerAsn 187
Db 373 CATGAACCCAAAT-----CTTCAGAGAGAGGGGTGTTTCAATAGATTACTGGAACTCT 426

Qy 188 SerArgLysAsnTrpAsnAspIleProCysPheTyrSerMetProTrpIleCysGluMet 207

Db 427 TCGAATGGCGCTGGAATGATGTTTCTGTGATAGTAACACAATTCATATGTGAATG 486
Qy 208 ProGluile 210
Db 487 AAGNAGATT 495

RESULT 13
US-09-111-470-1
; Sequence 1, Application US/091111470
; Patent No. 6277959
; GENERAL INFORMATION:
; APPLICANT: Valladeau, Jenny
; APPLICANT: Ravel, Odile
; APPLICANT: Bates, Elizabeth E.M.
; APPLICANT: Ford, John
; APPLICANT: Saeland, Sem
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Membrane Protein Genes;
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,470
; FILING DATE: 08-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,080
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SF0695
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 242..952
; US-09-111-470-1

Alignment Scores:
Pred. No.: 5.09e-31 Length: 1104
Score: 325.50 Matches: 72
Percent Similarity: 49.31% Conservative: 35
Best Local Similarity: 33.18% Mismatches: 101
Query Match: 27.61% Indels: 9
DB: 3 Gaps: 4

US-10-812-620-2 (1-214) x US-09-111-470-1 (1-1104)

Qy 1 MetAsnSerThrLysSerProAlaSerHisThrCluArgGlyCysPheLysAsnSer 20
Db 302 ATCAACACAGCCCTCTTCTCGAGCTTCCAGGAGGAGGACTGCCCTCTCAAAAGTAATACC 361

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QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeu-----SerGly 37
Db 362 GGATTCCTCCCAAGCTGTTGGCTGCACGTTGATATTTTCTGCTATTGGCAATCTCA 421
QY 38 CysPheIleThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeu 57
Db 422 TTCCTTATTGCTTTGCTCATTTCTTCAAAATATTTCTCAGCTTCTTGGAAAAAAGACT 481
QY 58 GlnProHisArgAsnIleLeuSerGluSerGlu-----AlaSerGly 74
Db 482 ACAAAAGAGCTGGTTCATACACATTTGGAGTGTGTGAAAAAAATATGCCCTGGAAGAG 541
QY 75 SerValLysAsnCysCysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePhe 94
Db 542 ACAGCTGGAGCTGTGGCCCAAGAAATGGAGTCAATTTAGTTCACACTGCTACTTTATT 601
QY 95 SerThrThrLeuThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHis 114
Db 602 TCTACTGAATCAGCATCTTGGCAAGACAGTGCAGAGGACTGTGCTAGATGGAGGCTCAC 661
QY 115 LeuValValIleAspThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 134
Db 662 CTGCTGGTGATAAACAACACTCAAGAGAGCAGAGTTCATCTCCAGAAATCTGCAAGAGAA 721
QY 135 LysGluPheTyrIleGlyLeuThrAspGlnValValGlnGlyGlnTrpValAsp 154
Db 722 TCTGCTTATTGTTGGTCTCTCAAGGTCAGTTTGTGAGATGATGAAGATC 946
QY 155 AspThrProPheThrGluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleVal 174
Db 782 CAGACACCATACAAATGAAAGTTCACATCTTGGCATCCACGTCGAGCCCGATGAT----- 835
QY 175 LeuValGluAspCysAlaThrIleArg---AspSerSerAsnSerArgLysAsnTrpAsn 193
Db 836 CCCAATGAGCGCTGGTGTGCTAAATTTTCTGTAATCACCACCAAGATGGGGCTGGAAT 895
QY 194 AspIleProCysPheTyrSerMetProTrpIleCysGluMetProGluIle 210
Db 896 GATGTTAATTGCTTGGTCTCTCAAGGTCAGTTTGTGAGATGATGAAGATC 946
RESULT 14
US-09-862-802A-1
; Sequence 1, Application US/09862802A
; Patent No. 6756478
; GENERAL INFORMATION:
; APPLICANT: Valladeau, Jenny
; APPLICANT: Ravel, Odile
; APPLICANT: Bates, Elizabeth Ester Mary
; APPLICANT: Ford, John
; APPLICANT: Lebecque, Serge J.E.
; APPLICANT: Saeland, Sem
; TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
; FILE REFERENCE: SF0695 B
; CURRENT APPLICATION NUMBER: 2001-05-22
; PRIOR FILING DATE: 2001-05-22
; PRIOR FILING DATE: 1997-07-09
; PRIOR FILING DATE: 1997-07-09
; PRIOR FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: mammalian nucleic acid and protein
; NAME/KEY: CDS
; LOCATION: (242)..(952)
; OTHER INFORMATION:
US-09-862-802A-1
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Alignment Scores:
Pred. No.: 5,098-31 Length: 1104
Score: 325.50 Matches: 72
Percent Similarity: 49.31% Conservative: 35
Best Local Similarity: 33.18% Mismatches: 101
Query Match: 27.61% Indels: 9
DB: 4 Gaps: 4
US-10-812-620-2 (1-214) x US-09-862-802A-1 (1-1104)
QY 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 302 ATCAACACAGCGCTCTTCTGCAGCTTCCCAAGAGAGACTGCCCTCTCTCAAAAGTAAATACC 361
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeu-----SerGly 37
Db 362 GGATTCCTCCCAAGCTGCTTTGGTGCCTCACTGTTGATATTTTCTGCTATTGGCAATCTCA 421
QY 38 CysPheIleThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeu 57
Db 422 TTCCTTATTGCTTTGCTCATTTCTTCAAAATATTTCTCAGCTTCTTGGAAAAAAGACT 481
QY 58 GlnProHisArgAsnIleLeuSerGluSerGlu-----AlaSerGly 74
Db 482 ACAAAAGAGCTGGTTCATACACATTTGGAGTGTGTGAAAAAAATATGCCCTGGAAGAG 541
QY 75 SerValLysAsnCysCysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePhe 94
Db 542 ACAGCTGGAGCTGTGGCCCAAGAAATGGAGTCAATTTAGTTCACACTGCTACTTTATT 601
QY 95 SerThrThrLeuThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHis 114
Db 602 TCTACTGAATCAGCATCTTGGCAAGACAGTGCAGAGGACTGTGCTAGATGGAGGCTCAC 661
QY 115 LeuValValIleAspThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 134
Db 662 CTGCTGGTGATAAACAACACTCAAGAGAGCAGAGTTCATCTCCAGAAATCTGCAAGAGAA 721
QY 135 LysGluPheTyrIleGlyLeuThrAspGlnValValGlnGlyGlnTrpValAsp 154
Db 722 TCTGCTTATTGTTGGTCTCTCAAGGTCAGCGAGTGCAGACATTTGGCAATGGGTTGAT 781
QY 155 AspThrProPheThrGluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleVal 174
Db 782 CAGACACCATACAAATGAAAGTTCACATCTTGGCATCCACGTCGAGCCCGATGAT----- 835
QY 175 LeuValGluAspCysAlaThrIleArg---AspSerSerAsnSerArgLysAsnTrpAsn 193
Db 836 CCCAATGAGCGCTGGTGTGCTAAATTTTCTGTAATCACCACCAAGATGGGGCTGGAAT 895
QY 194 AspIleProCysPheTyrSerMetProTrpIleCysGluMetProGluIle 210
Db 896 GATGTTAATTGCTTGGTCTCTCAAGGTCAGTTTGTGAGATGATGAAGATC 946
RESULT 15
US-09-489-847-119
; Sequence 119, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
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; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 2059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-847-119

Alignment Scores:
Pred. No.: 5,33e-29 Length: 2059
Score: 313.00 Matches: 80
Percent Similarity: 56.93% Conservative: 35
Best Local Similarity: 39.60% Mismatches: 72
Query Match: 26.55% Indels: 16
DB: 4 Gaps: 4

US-10-812-620-2 (1-214) x US-09-489-847-119 (1-2059)

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Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 105 CAGCTGATACCTTCGGTTATTGCTGTAGTTTCACTTCTTCGGTGTCTGTTTATT 164
Qy 41 ThrArgCysValValThrTyr-----ArgSerSerGlnIleSerGly---Gln 55
Db 165 GCAAAGTTGTTGGTGACTCATCAACAACCTTTTCACGCTGTAAGAGAGGCACAGGAGTGCAC 224
Qy 56 AsnLeuGlnProHis-----ArgAsnIleLysGluLeuSerCysTyrSerGlu-Al 72
Db 225 AAGTTAGAGCACCATGCAAGACTCAAAATGCAATCAAGAGAAATCAGAACTGAAAAGTTGC 284
Qy 72 aserGlySerValLysAsnCysProLeuAsnTrpLysHisTyrGln-SerSerCysT 92
Db 285 TGAAGGGAGCACCTGGAACTGTTGCTTATTGCTGAGAAACCTTCCAGTTCCAACTGCT 344
Qy 92 Yr-PhePheSerThrThrLeuThrTrpSerSerLeuLys-AsnCysSerAspMe 111
Db 345 ATTTTCTCTCTTACTGACAACAAGACGTGGGCTGAGAGTTGAAAGGAACCTGTTCAGGGAT 404
Qy 111 tGlyAlaHisLeuValValIleAspThrGlnGluGlnGluPheLeuPheArgThrLy 131
Db 405 GGGGGCCCATCTGATGACCATCAGCAGCGAAGCTGAGCAGAACTTTATTATTCACTTCT 464
Qy 131 sProLysArgLysGluPheTyrIleGlyLeuThrAspGlnValValGluGlyGlnTrpGl 151
Db 465 GGATAGACGGCTTCTCTATTTCCTTGGACTTGTAGATGAGAAATGCCAAAGGTCAAGTGGCG 524
Qy 151 nTrpVal-AspAspThrProPhe-ThrGluSerLeuSerPheTrpAspAlaGlyGluPro 170
Db 525 TTGGGTGGGACCAGACGCCATTAAACCCACCCAGAGTATTCTGGCATAGAATGAACCC 584
Qy 171 AsnAsnIleValLeuValGluAspCysAlaThrIleArgAspSerSerAsnSerArgLys 190
Db 585 GACAAC---TYTCAGGGAGAAAACGTGTTCTCTGG--TCTTATAACCAAGATAAATGG 639
Qy 191 AsnTrpAsnAspIleProCysPheTyrSerMetProTrpIleCysGluMetPro 208
Db 640 GCCTGGGAATGATGTTCTTGTAACTTTGAAGCAAGTAGGATTGTAAATACCT 693
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Search completed: June 9, 2005, 16:23:34
Job time : 194 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2005, 09:46:10 ; Search time 4143 Seconds
(without alignments)
2502.876 Million cell updates/sec

Title: US-10-812-620-2

Perfect score: 1179

Sequence: 1 MNSTKSPASHHTGCGFKNS.....IPCFYSPWICEMPEISPLD 214

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0			0.5
Ygapop 6.0			7.0
Delop 6.0			7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10812620/runat_07062005_124336_3244/app_query.fasta_1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10812620 @CGN 1.1 4200 @runat_07062005_124336_3244 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*

2: gb_btg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1179	100.0	1606	10_ BC003218	Mus muscu
2	1179	100.0	2517	10_ AB024717	Mus muscu
3	1149	97.5	2517	6_ E54035	Novel C lec
4	1149	97.5	2517	6_ BD094039	A novel C

ALIGNMENTS

RESULT 1	BC003218	1606 bp	linear	ROD 29-JUN-2004
LOCUS	BC003218	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, mRNA (cdna clone MGC:5682 IMAGE:3158063), complete cds.		
DEFINITION	BC003218	IMAGE:3158063, complete cds.		
ACCESSION	BC003218	GI:13096843		
VERSION	BC003218.1			
KEYWORDS	MGC.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1 (bases 1 to 1606)			
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheet, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,			

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
JOURNAL
PUBMED
AUTHORS
JOURNAL

REFERENCE
2 (bases 1 to 1606)

Strausberg,R.

Direct Submission

Submitted (20-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: ang@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleaged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 6 Row: 1 Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9910161.

FEATURES

source

1..1606
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="MGC:5692 IMAGE:3158063"
/tissue_type="Mammary tumor. C3(1) -Tag model. Infiltrating
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

gene

1..1606
/gene="Clec4e9"
/note="synonym: Mincle"
/db_xref="LocusID:56619"
/db_xref="MGI:1861232"
82..726
/gene="Clec4e9"
/codon_start=1
/product="C-type lectin, superfamily member 9"

CDS

/protein_id="AAH03218.1"
/db_xref="GI:13096844"
/db_xref="LocusID:56619"
/db_xref="MGI:1861232"
/translation="WNSTKSPASHHTGCKFNKSOVLWNTIAGSILFLSGCITRCV
VYRSQISQGNLQPHRNKELSCYSEASGVKNCPLNWKHYQSCFFSYTITLWS
SLKNCSDGALHLVIDTQEEQFLRTKPKRKEFYIGLTDQVGVGQWQVDDTPTFE
SLSPWDGEPNNVLVEDCATIRDSNRKNNDIPCFYSMPWICEMPEISPLD"

ORIGIN

Alignment Scores:

Pred. No.: 3,38e-111 Length: 1606
Score: 1179.00 Matches: 214
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 10

US-10-812-620-2 (1-214) x BC003218 (1-1606)

QY 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
DB 82 ATGAATTCAACCAATCGCTCCATCCACACAGAGAGAGGATGTTTCAAAAATCC 141
QY 21 GlnValLeuSerTrrThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPhe 40
DB 142 CAAGTGCTCTCTCTGGACGATAGCCGGGCGCTCCATCTCTCAGTGGCTTTTCATC 201
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAenLeuGlnProHis 60
DB 202 ACCAGATGTGTCTAACAATATCGAGCTCTCAATTCGGGCGAGACTTACAGCCACAT 261
QY 61 ArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 80
DB 262 AGAATAATTAAGGAGCTTTCTCTGCTACAGTGAGGCATCAGGTTCAGTCAAGAAATGCTGT 321
QY 81 ProLeuAenTrrLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeuThr 100
DB 322 CCTTTGAATCGAAACATTAATCTAGTTGTATTATTTTCTCTACGACCACTTGACC 381
QY 101 TrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
DB 382 TGGTCATCAAGTTTAAAGAAATTCCTCAGACATGGGGCTCACCCTGGTGTATCGACACA 441
QY 121 GlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
DB 442 CAGGAAGAGCAGGAATTCCTTTTCGCACAAAACCTAAAGAGAAAGAGTTTATATGGA 501
QY 141 LeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
DB 502 CTGACAGACACAGGTGGTGGAGGTCAGTGGCAATGGGTGGATGATACACCTTTTCACAGAG 561
QY 161 SerLeuSerPheTrrAspAlaGlyGluProAenAenIleValLeuValGluAspCysAla 180
DB 562 TCCCTGAGCTCTGGGATGCTGGGAGGCCCAACAATATAGTTTGGTGGAGGACTGTGCC 621
QY 181 ThrIleArgAspSerSerAsnSerArgLysAenTrpAenAspIleProCysPheTyrSer 200
DB 622 ACCATAAGGAGCTCTTCAAACTCCAGGAAGAACTGGAAATGATATACCTCTTCTACAGT 681
QY 201 MetProTrrLysCysGluMetProGluIleSerProLeuAsp 214
DB 682 ATGCTTGGATTGTGAGATGCCAAATAAGTCTCTCTGGAC 723

RESULT 2

AB024717

LOCUS

DEFINITION

Mus musculus mRNA for macrophage C-type lectin Mincle, complete

cds.

AB024717

VERSION

AB024717.1 GI:5821285

KEYWORDS

Mincle; macrophage C-type lectin Mincle.

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 2517)

Akira,S. and Matsumoto,M.

Direct Submission

Submitted (09-MAR-1999) Shizuoka Akira, Osaka University, Department

of Host Defense, Research Institute for Microbial Diseases; 3-1

Yamada-oka, Suita, Osaka 565-0871, Japan

Yamada-oka, Suita, Osaka 565-0871, Japan

Yamada-oka, Suita, Osaka 565-0871, Japan

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Yamada-oka, Suita, Osaka 565-0871, Japan

Yamada-oka, Suita, Osaka 565-0871, Japan

Yamada-oka, Suita, Osaka 565-0871, Japan

Qy	141	LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu	160
Db	544	CTCACACACAGGCTGGTGGAGGGTCACTGGCAATGGGAGGATGATACACCTTTACACAG	603
Qy	161	SerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValIleuValGluAspCysAla	180
Db	604	TCCCTGACCTTCGGGATGCTGGGGAGCCCAACATATAGTTTGGTGGAGGACTGTGCC	663
Qy	181	ThrIleArgAspSerSerAsnSerArgIleAsnTrpAsnAspIleProCysPheTySer	200
Db	664	ACCATAGGGACCTCTTCAACTCCAGAGAGACTGGATGATANTATCCCTGTTTCTACAGT	723
Qy	201	MetProTrpIleCysGluMetProGluIleSerProLeuAsp	214
Db	724	ATGCCTTGGATTTGTGAGATGCCAGAAATAAGTCCTCAGGAC	765
RESULT 4			
BD094039			
LOCUS			
DEFINITION			
A novel C-type lectin and its genes.			
ACCESSION			
BD094039			
VERSION			
BD094039.1 GI:22639627			
KEYWORDS			
WO 0127271-A/1.			
SOURCE			
Mus sp.			
ORGANISM			
Mus sp.			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
1 (bases 1 to 2517)			
Akira,S. and Matsumoto,M.			
A novel C-type lectin and its genes			
Patent: WO 0127271-A 1 19-APR-2001;			
JAPAN SCIENCE AND TECHNOLOGY CORP,SHIZUO AKIRA,MAKOTO MATSUMOTO			
OS Mus sp. (mouse)			
PN WO 0127271-A/1			
PD 19-APR-2001			
PF 02-OCT-2000 WO 2000JP006820			
PR 15-OCT-1999 JP 99P 293724			
PI SHIZUO AKIRA,MAKOTO MATSUMOTO			
PC C12N15/12,C07K14/47,C12Q1/68,A61K38/17,A61P31/00,A61P37/04,PC			
A61P43/00			
CC			
FEATURES			
source			
1..2517			
/organism="Mus sp."			
/mol_type="genomic DNA"			
/db_xref="taxon:10095"			
ORIGIN			
Alignment Scores:			
Pred. No.:	6.95e-108	Length:	2517
Score:	1149.00	Matches:	209
Percent Similarity:	98.13%	Conservative:	1
Best Local Similarity:	97.66%	Mismatches:	4
Query Match:	97.46%	Indels:	0
DB:	6	Gaps:	0
US-10-812-620-2 (1-214) x BD094039 (1-2517)			
Qy	1	MetAsnSerThrTySerProAlaSerHisThrGluArgGlyCysPheLysAsnSer	20
Db	124	ATGAATTCAACCAATCGCTCGCATCCACCACACAGAGAGAGATGCTTCAAAACTCC	183
Qy	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
Db	184	CAAGTGCTCTCTGGAGCATAGCGGGCCCTCCATCTCTGTTCTCAGTGGCTGTTTCATC	243
Qy	41	ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis	60
Db	244	ACCAGATGTGTGCTGTAACATATCGCAGCTCTCAAAATTTCCGGCGAGAACTTACAGCCACAT	303
Qy	61	ArgAsnIleLysGluLeuSerCysTyTrpSerGlnAlaSerGlySerValLysAsnCysCys	80

/translation="MNSTKSPASHHTEECFKNQVLSTWVWAGASILFLSVCFITRCV
VTYHFOYGGKLOPHKTIKELSCYLEAGSVKNCCLPNWKFQSSCFYFSTLLSM
LSSKNSDMGAHLVAVTWEEQFLFRTPKKEFYIGLTDQVVEGQWAVDDTPT
ESLSFMDAGEPNNVFVEDCATMRDSSNPRKNWVDVSCFFSMPVICEMPEISPLD"

ORIGIN

Alignment Scores:
Pred. No.: 2,73e-98 Length: 730
Score: 1049.50 Matches: 190
Percent Similarity: 93.49% Conservative: 11
Best Local Similarity: 88.37% Mismatches: 13
Query Match: 89.02% Indels: 1
DB: 10 Gaps: 1

US-10-812-620-2 (1-214) x AY363175 (1-730)

Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 51 ATGAATTCACCAATCGCTGCATCACACACAGAGAGAGATGCTTCAAAACTCC 110
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 111 CAAGTGCTTCATGACGAGTGGCTGGGCGCTCCATCGTCTCAGTGCTGTTCATC 170
Qy 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln--AsnLeuGlnPro 59
Db 171 ACCAGATGCTGTGTAACATATACAGATTTTCAAAATTTATGGCAGAGAGATTACAGCCA 230
Qy 60 HisArgAsnIleLysGluLeuSerCysTyTrpSerGluAlaSerGlySerValLysAsnCys 79
Db 231 CATAAACTATTAGGAGCTTCTCTGCTACCTTGAAGCATCAGGTTCAGTCAAGATTGC 290
Qy 80 CysProLeuAsnTrpLysHisTyArgGlnSerCysTyTrpPhePheSerThrThrLeu 99
Db 291 TGCCTTTGAAGTGAACATTTTCAGTCTAGTGTCTACTTTTCTACACACCTTA 350
Qy 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValLysAsp 119
Db 351 TCCTGGCTATCAAGCTAAAGATTTGCTCAGACATGGGGCTCACCTGGTGTATCAAC 410
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyIle 139
Db 411 ACATGGAAGAGCAGGAATTCCTTTTTCGACAAACCCAGAAAGAGATTTTACAT 470
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpValAspAspThrProPheThr 159
Db 471 GGACTGACAGACCAAGTTGTGAGGGTCAGTGGCGATGGGTGGATGATACACCTTTTACA 530
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 531 GAGTCCCTGAGCTTCTGGATGCTGGAGAGCCCAATACATAGTTTTTGTGGAGGACTGT 590
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTy 199
Db 591 GCCACCATGAGGAGTCTTCAAAACCCAGGAGAACTGGATGATGATCTGTTCTTCTC 650
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 651 AGTATGCTTGGATTTGTGAGATGCCAGAAATAAGTCTCTTGGAC 695

RESULT 6
BC000715
LOCUS
DEFINITION Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9, mRNA (cDNA clone MGC:1246 IMAGE:3507103), complete cds.
ACCESSION BC000715
VERSION BC000715.2 GI:33875777
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 927)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheet, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shrivchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smillius, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 927)
Strausberg, R.
Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:12653848.
Contact: MGC help desk
Email: cgapba-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadon@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Helton and Michelle Whiting

REMARK
COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 7 Row: 1 Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657332.

FEATURES
source

1. .927
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:1246 IMAGE:3507103"
/tissue_type="Kidney, renal cell adenocarcinoma"
/clone_lib="NIH MGC 14"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
1. .927
/gene="CLECSEF9"
/note="synonym: MINCLE"
/db_xref="LocusID:26253"
84_..743
/gene="CLECSEF9"
/codon_start=1
/product="C-type lectin, superfamily member 9"
/protein_id="AAH00715.1"
/db_xref="GI:12653849"
/db_xref="LocusID:26253"
/translation="MNSSKSECTQCTGRCFSSQMLWTVAGIPILFSACFITRCVV
TFRTFTCDKKFQLPENFTLSCYNGSVKNCCLPNWKFQSSCFYFSTLLSM
LSSKNSAMGAHLVAVINSQEEQFLSYKKPKMREFFIGLSDQVVEGQWAVDDTPTK
SLSFVDVGEPNNTATLEDCAATMRDSSNPRQWMDVTCLNRYFRICEMVGINLKGKS

gene

CDS

ORIGIN	L"	Incyte Genomics, Inc. (US)
Alignment Scores:	7.51e-70	Location/Qualifiers
Pred. No.:	774.00	1..968
Score:	774.00	/organism="Homo sapiens"
Percent Similarity:	79.07%	/mol_type="unassigned DNA"
Best Local Similarity:	66.51%	/db_xref="taxon:9606"
Query Match:	65.65%	/note="Incyte ID No: 1521513CB1"
Indels:	2	
Gaps:	2	
US-10-812-620-2 (1-214) x BC000715 (1-927)		
Qy	1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer	20
Db	84 ATGAATCTCATTAATCATCTCTGAACACAATGCACAGAGAGGATGCTTC---TCTTCC	140
Qy	21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPhele	40
Db	141 CAAATGTTCTTATGGACTGTGCTGGATCCCATCTATTCTCAGTGCCTGTTTCATC	200
Qy	41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro	59
Db	201 ACCAGATGTGTGTGACATTTCCGATCTTTCAACCTGTGATCAGAAAAAGTTTCAGCTA	260
Qy	60 HisArgAsnIleLysLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys	79
Db	261 CCTGAGAATTTACAGAGCTCTCTGCTACAATATTATGGATCAGGTTTCAGTCAAGAAATGT	320
Qy	80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu	99
Db	321 TGTCCATTGAATCGGGAATATTTTCAATCCAGCTGCTACTCTTTTCTACTGACACCAT	380
Qy	100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValleasp	119
Db	381 TCCTGGCGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC	440
Qy	120 ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle	139
Db	441 TCACAGGAGGACAGGAATCTTCTTCTACAGAAACCTTAAATAGAGAGTTTTTATT	500
Qy	140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr	159
Db	501 GGACTGTCAGACAGAGTTGTCAGGGTCAGTGGCAATGGTGGCGCACACCTTTTGACA	560
Qy	160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys	179
Db	561 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACACATAGCTACCTGGAGGACTGT	620
Qy	180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr	199
Db	621 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATTTGGAATGATGTAACCTGTTTCTC	680
Qy	200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp	214
Db	681 AATTATTTTCGGATTGTGAAATGGTAGGAATAAATCTTTTGAAAC	725
RESULT 7		
AX083498		
LOCUS	AX083498	968 bp DNA linear PAT 28-FEB-2001
DEFINITION	Sequence 40 from Patent WO0112662.	
ACCESSION	AX083498	
VERSION	AX083498.1	GI:13185308
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 Lal, P., Yue, H., Tang, Y.T., Bandman, O., Burford, N., Azimzai, Y.,	
JOURNAL	Baughn, M.R., Lu, D.A. and Patterson, C.	
	Membrane associated proteins	
	Patent: WO 0112662-A 40 22-FEB-2001;	
FEATURES		
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ACCESSION	BD172543	
VERSION	BD172543.1	GI:28413845
KEYWORDS	JP 200223786-A/316.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 997)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: JP 2002223786-A 316 13-AUG-2002;
GENENTECH INC
COMMENT
OS Homo sapiens (human)
PN JP 2002223786-A/316
PD 13-AUG-2002 JP 2001385135
PF 18-DEC-2001 JP 60/059115,17-SEP-1997 US 60/059184 PR
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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
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Pred. No.: 8.18e-70 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 6 Gaps: 2
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DEFINITION
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the same.
VERSION
BD172862.1 GI:28414166
KEYWORDS
JP 2002238586-A/316.
SOURCE
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 997)
AUTHORS
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: JP 2002238586-A 316 27-AUG-2002;
GENENTECH INC
COMMENT
OS Homo sapiens (human)
PN JP 2002238586-A/316
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385205
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
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24-NOV-1997 US	60/066453, 25-NOV-1997 US	60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI		
JIAN ZHENG,		
PI JEAN YUAN		
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC	C12N5/10,	
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Percent Similarity:	79.07%	Conservative: 27
Best Local Similarity:	66.51%	Mismatches: 43
Query Match:	65.65%	Indels: 2
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Secreted and transmembrane polypeptides and nucleic acids encoding		
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VERSION		
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ORGANISM		
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE		
1 (bases 1 to 997)		
AUTHORS		
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and		
Yuan, J.		
TITLE		
Secreted and transmembrane polypeptides and nucleic acids encoding		
the same		
JOURNAL		
Patent: JP 2002238587-A 316 27-AUG-2002;		
GENENTECH INC		
COMMENT		
OS	Homo sapiens (human)	
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WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI		
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PI JEAN YUAN		
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ORIGIN

Alignment Scores:

Pred. No.: 8.18e-70 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
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US-10-812-620-2 (1-214) x BD173181 (1-997)

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BD173500

LOCUS

DEFINITION

Secreted and transmembrane polypeptides and nucleic acids encoding

the same.

ACCESSION

BD173500.1

VERSION

BD173500 997 bp DNA linear PAT 18-FEB-2003

Secreted and transmembrane polypeptides and nucleic acids encoding

the same.

BD173500

BD173500.1 GI:28414831

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JP 2002238588-A/316.

Homo sapiens (human)

Homo sapiens

1 (bases 1 to 997)

Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and

Yuan,J.

Secreted and transmembrane polypeptides and nucleic acids encoding

the same

Patent: JP 2002238588-A 316 27-AUG-2002;

GENENTECH INC

OS Homo sapiens (human)

PN JP 2002238588-A/316

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385315

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21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR

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07-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR

17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR

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24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066640 PR

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC

C12N5/10,

PC C12P21/02, C12P21/08, (C12N1/19, C12R1/645), (C12N1/21, C12R1/19),

PC (C12N5/10, C12R1/91), C12N15/00, C12N5/00, (C12N5/00, C12R1/91) CC

Secreted and transmembrane polypeptides and nucleic CC acids

encoding the same

FH Key Location/Qualifiers

FT source 1..997

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FEATURES

source

1..997

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ORIGIN

Alignment Scores:

Pred. No.: 8.18e-70 Length: 997

Score: 774.00 Matches: 143

Percent Similarity: 79.07% Conservative: 27

Best Local Similarity: 66.51% Mismatches: 43

Query Match: 65.65% Indels: 2

DB: 6 Gaps: 2

US-10-812-620-2 (1-214) x BD173500 (1-997)

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Db 106 ATGAATTCATCTAAATCATCTGAAACACAATGCACAGAGAGATGCTTC---TCTCC 162

QY	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheIleuSerGlyCysPheIle	40
Db	163	CAAAATGTTCTTAGGACTGTTCTGGATGCCCATCTTAATTTCTCAGTGCCTGTTTCATC	222
QY	41	ThrArgCysValValThrTrpArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro	59
Db	223	ACCAGATGTTGTGACATTTCCGATCTTTCAAACTGTGATGAGAAAAAGTTTCAGCTA	282
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Db	283	CCTGAGAATTTACAGAGCTCTCTGCTACAAATATGATCAGGTTTCAGTCAAGAATTGT	342
QY	80	CysProLeuAsnTrpLysHisTrpGlnSerSerCysTrpPhePheSerThrThrLeu	99
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QY	100	ThrTrpSerSerLeuIysAsnCysSerAspMetGlyAlaHisLeuValIleAsp	119
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QY	120	ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTrile	139
Db	463	TCACAGGAGGAGCAGGAATTCCTTCTCTACAGAAACCTAAATAGAGAGATTTTATT	522
QY	140	GlyLeuThrAspGlnValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr	159
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QY	160	GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys	179
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QY	180	AlaThrIleArgAspSerSerAsnSerArgThrLysAsnTrpAsnAspIleProCysPheTrp	199
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.		
TITLE	Secretory and transmembrane polypeptide and nucleic acid encoding the same		
JOURNAL	Patent: JP 2002253280-A 316 10-SEP-2002; GENENTECH INC		
COMMENT	OS Homo sapiens (human) PN JP 2002253280-A/316 PD 10-SEP-2002 PF 18-DEC-2001 JP 2001385319 PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR		

24-OCT-1997 US	60/063045, 24-OCT-1997 US	60/063128 PR
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24-NOV-1997 US	60/066453, 25-NOV-1997 US	60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI		
JIAN ZHENG,		
PI JEAN YUAN		
PC C12N15/09, A61K45/00, A61P1/00, A61P13/12, A61P17/00, A61P17/06, PC		
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PC C12N1/19, C12N1/21, C12N5/10//A61K38/00, A61K39/395, A61K39/395,		
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PC C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19), (C12N5/10,		
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Secretory and transmembrane polypeptide and nucleic acid CC		
encoding the same		
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source		
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Score:	774.00	Matches: 143
Percent Similarity:	79.07%	Conservative: 27
Best Local Similarity:	66.51%	Mismatches: 43
Query Match:	65.65%	Indels: 2
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QY	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db	163	CAAAATGTTCTTAGGACTGTTCTGGATCCCCATCTTATTTCTCAGTGCCTGTTTCATC 222
QY	41	ThrArgCysValValThrTrpArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
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ACCESSION AR410914
VERSION AR410914.1 GI:40162414
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 997)
AUTHORS Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,
Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,
Kijavini, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,
Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6635468-A 376 21-OCT-2003;
FEATURES Location/Qualifiers
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Best Local Similarity: 65.65% Indels: 2
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Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLysGlyCysPheIle 40
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ACCESSION AR439278
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SOURCE Unknown.
ORGANISM Unknown.
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AUTHORS Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,
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Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,
Kijavini, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,
Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6664376-A 376 16-DEC-2003;
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Alignment Scores: 8.18e-70 Length: 997
Pred. No.: 774.00 Matches: 143
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Best Local Similarity: 65.65% Indels: 2
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Db 163 CAAATGTTCTTATGGAGCTGTGCTGGATCCCATCTATTTCTCAGTCGCTGTTTCATC 222
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Db     463  TCACAGGAGGAGCAGGAATTCCTTCTACAGAAACCTAAATAGAGAGTTTTTATT 522

QY     140  GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThr 159
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QY     180  AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db     643  GCCACCATGAGAGACTCTTCAAAACCCCAAGGCAAAATTTGAATGATGTAACTGTTTCCTC 702

QY     200  SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 997)
AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L., Mather,J.P.,
        Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: US 6686451-A 376 03-FEB-2004;
FEATURES Location/Qualifiers
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Pred. No.: 8.18e-70 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 6 Gaps: 2
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US-10-812-620-2 (1-214) x AR473298 (1-997)

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QY     21  GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
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Job time : 4161 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Perfect score: 1179

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Maximum Match 100%

Listing first 45 summaries

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5	774	65.6	997	2 AAX52274	Aax52274 Protein P

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19	774	65.6	997	8 ACD25062	Accd25062 Human sec
20	774	65.6	997	8 ACF00111	Accf00111 Human sec
21	774	65.6	997	8 ACA72168	Acca72168 Novel hum
22	774	65.6	997	8 ACD04692	Accd04692 Novel hum
23	774	65.6	997	8 ACD18153	Accd18153 Human sec
24	774	65.6	997	8 ACD08160	Accd08160 Human sec
25	774	65.6	997	8 ABX71765	Abx71765 Human CDN
26	774	65.6	997	8 ACA88594	Acca88594 Novel hum
27	774	65.6	997	8 ACA70036	Acca70036 Human sec
28	774	65.6	997	8 ACD12258	Accd12258 Novel hum
29	774	65.6	997	8 ACC74173	Acc74173 Human sec
30	774	65.6	997	8 ACD15801	Accd15801 Human sec
31	774	65.6	997	8 ACD25369	Accd25369 Novel hum
32	774	65.6	997	8 ACD17846	Accd17846 Human sec
33	774	65.6	997	8 ACC88133	Acc88133 Human sec
34	774	65.6	997	8 ACD21487	Accd21487 Human sec
35	774	65.6	997	8 ACD18554	Accd18554 Human sec
36	774	65.6	997	8 ACH07096	Ach07096 Human sec
37	774	65.6	997	8 ABX98164	Abx98164 Human CDN
38	774	65.6	997	8 ACD13915	Accd13915 Human PRO
39	774	65.6	997	8 ACD09695	Accd09695 Human sec
40	774	65.6	997	8 ACC88440	Acc88440 Human sec
41	774	65.6	997	8 ACD21180	Accd21180 Human sec
42	774	65.6	997	8 ABX75552	Abx75552 Human CDN
43	774	65.6	997	8 ABX97755	Abx97755 Human PRO
44	774	65.6	997	8 ACA97231	Acca97231 Novel hum
45	774	65.6	997	8 ACA57694	Acca57694 Human PRO

ALIGNMENTS

RESULT 1
AAF86349
ID AAF86349 standard; CDNA; 2517 BP.

AC AAF86349;

XX 23-JUL-2001 (first entry)

DT Murine cDNA encoding C-type lectin Mincle.

DE Mouse; Mincle; C-type lectin; antiinflammatory; macrophage; inflammation; immune disorder; nuclear factor interleukin 6; NF-IL6; ss.

XX Mus sp.

XX Key Location/Qualifiers
FH CDS 124..768
FT /*tag= a

FT /product= "Mincle"

FT /note= "C-type lectin"

XX WO200127271-A1.

XX 19-APR-2001.

XX 02-OCT-2000; 2000WO-JP006820.

XX 15-OCT-1999; 99JP-00293724.

XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX Akira S, Matsumoto M;
XX WPI; 2001-273771/28.
DR P-PSDB; AAB97225.
XX
PT New macrophage activating C-type lectin for the treatment of immune
XX disorders and inflammation.
XX
PS Claim 4; Fig 4; 60pp; Japanese.
XX
CC This invention relates to a C-type lectin, termed Mincle, which is formed
CC from a transcriptional target gene of nuclear factor interleukin 6 (NF-
CC IL6). Mincle is a macrophage activating protein which can be used in the
CC treatment of immune disorders, and inflammation. Compositions containing
CC the protein have immunomodulatory and antiinflammatory activity. The
CC present sequence represents murine cdna encoding Mincle
XX
SQ Sequence 2517 BP; 756 A; 533 C; 463 G; 765 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.19e-115 Length: 2517
Score: 1179.00 Matches: 214
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-812-620-2 (1-214) x AAF86349 (1-2517)

QY 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
DB 124 ATGAATTCACCAAAATCGCTGCATCCACACACAGAGAGGATGCTTCAAAAACCTCC 183
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
DB 184 CAAGTGCTCTCTGGACGATAGCCGGGGCTCCATCTGTTCTCAGTGGCTGTTTCATC 243
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
DB 244 ACCAGATGTGCTTAACATATCGCAGCTCTCAAAATTCGGGGCAGAACTTACAGCCACAT 303
QY 61 ArgAsnIleGlyGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCysCys 80
DB 304 AGAAATATTAAAGAGCTTTCCTGCTACGTAGGCGCATCAGGTTCAAGAAATTGCTGT 363
QY 81 ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr 100
DB 364 CTTTGAACCTGGAAACATTATCAATCTAGTTGTTATTTTCTTACGACAACTTGACC 423
QY 101 TrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
DB 424 TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGGCTCACCTGGTGGTTATCGACACA 483
QY 121 GlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheThrIleGly 140
DB 484 CAGGAAGACGACGAATTCCTTTTCGCACAAAACCTTAAAGAAAGAGTTTATATTGGA 543
QY 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
DB 544 CTGACAGACACAGGTGGTGAGGGTCAGTGGCAATGGGTGGATGATACACTTTCACAGAG 603
QY 161 SerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCysAla 180
DB 604 TCCCTGAGCTTCTGGGATGCTGGGGAGCCCAATATATAGTTTGGTGGAGGACTGTGCC 663
QY 181 ThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheThrSer 200
DB 664 ACCATAAGGAGCTCTTCAAACTCCAGGAAGAACTGGAATGATATACCTGTTTCTACAGT 723
QY 201 MetProTrpIleCysGluMetProGluIleSerProLeuAsp 214

DB 724 ATGCCTTGGATTGTGAGATGCCAGAAATAAGTCTCTGGAC 765
RESULT 2
AAF81743
ID AAF81743 standard; cDNA; 968 BP.
XX
AC AAF81743;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human membrane associated protein MEMAP-3 encoding cDNA.
XX
KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea; ss.
XX
OS Homo sapiens.
XX
PN WO200112662-A2.
XX
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US022315.
XX
PR 17-AUG-1999; 99US-0149641P.
XX
PR 09-NOV-1999; 99US-0164203P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
XX
DR WPI; 2001-168860/17.
XX
DR P-PSDB; AAB74697.
XX
PT Isolated polypeptide with a human membrane associated protein sequence is
PT useful for the diagnosis, prevention and treatment of cell proliferative,
PT autoimmune/inflammatory, neurological and gastrointestinal disorders.
XX
PS Example; Page 151; 173pp; English.
XX
CC AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders
CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated with
XX MEMAP
SQ Sequence 968 BP; 314 A; 197 C; 205 G; 252 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.35e-72 Length: 968
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27


```

RESULT 4
ID ADR41300 standard; cDNA; 990 BP.
AC ADR41300;
DT 07-OCT-2004 (first entry)
XX
DE Human CD-like molecule HYAM43 cDNA, SEQ ID NO:99.
XX
KW Human; CD-like molecule; cluster of differentiation; diagnosis;
KW prevention; immune disorder; immunodeficiency; autoimmune disorder;
KW blood-related disorder; haematological disorder; haemostatic disorder;
KW thrombolytic disorder; hyperproliferative disorder; cancer; tumour;
KW apocytic disorder; cardiovascular disorder; respiratory disorder;
KW angiogenic disorder; neovascularisation; neurological disorder;
KW endocrine disorder; reproductive system disorder; infectious disease;
KW gastrointestinal disorder; drug screening; tissue regeneration;
KW chemotaxis; gene therapy; antibody therapy; drug targeting;
KW chromosome mapping; forensic analysis; immunophenotyping; cytostatic;
KW haemostatic; tranquiliser; vulnerary; antiinflammatory; nephrotropic;
KW cardiac; antiallergic; anti-HIV; antirheumatic; antiarthritic;
KW antipsoriatic; immunosuppressive; vasotropic; nootropic; neuroprotective;
KW antithyroid; thyromimetic; gynaecological; virucide; hepatotropic;
KW antibacterial; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200226930-A2.
XX
XX 04-APR-2002.
XX
XX 25-SEP-2001; 2001WO-US029838.
XX
XX 26-SEP-2000; 2000US-0235484P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Birse CE;
XX
XX WPI; 2002-405050/43.
XX
XX P-PSDB; ADR41476.
XX
XX Novel polynucleotides and polypeptides useful for treating, preventing or
XX ameliorating cardiovascular, renal, neurovascular, and autoimmune
XX disorders.
XX
XX Claim 4; SEQ ID NO 99; 1243pp; English.
XX
XX The invention relates to 167 novel human CD (cluster of differentiation)-
XX like molecules (ADR41388-ADR41563) and to cDNAs encoding them (seqid:11)-
XX
XX Sequence 990 BP; 342 A; 192 C; 206 G; 249 T; 0 U; 1 Other;
XX
Alignment Scores:
Pred. No.: 1,39e-72 Length: 990
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 7 Gaps: 2
US-10-812-620-2 (1-214) x ADR41300 (1-990)
QY 1 MetAsnSerThrIysSerProAlaSerHisHisThrGluArgGlyCysPheIysAsnSer 20
Db 149 ATGAATTCATCTAAATCATCTGAAACACATGACACAGAGAGAGGATGCTTC---TCTTCC 205
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 206 CAAATGTTCTTATGGACTGTGTGGTGGATCCCATCTATTCTCATGTCCTGTTTCATC 265
QY 41 ThrArgCysValValThrTrpTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 266 ACCAGATGCTGTGTGACATTTCCGATCTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTA 325
QY 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
Db 326 CCTGAGAATTTTCACAGAGCTCTCTCTGTCTACAATATTGATGATCAGGTTCAAGAAATTGT 385
QY 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 386 TGTCCATTGAACTGGGAATATTTCATCCAGCTGCTACTCTCTTTCTACTGACACCAATT 445
QY 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 446 TCTTGGGGTAAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCCTGGTGTATCAAC 505
QY 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 506 TCACAGGAGGAGCAGGAATTCCTTCTCTACAAGAAACCTAAATGAGAGAGTTTTTATT 565
QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 566 GGACTGTGAGACCAAGGTTGTGAGGGTCAGTGGCAATGGGTGGAGCGGCACACCTTTGACA 625
QY 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 626 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACACATAGCTACCTCGGAGGACTGT 685
QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 686 GCCACCATGAGAGACTCTTCAACCAAGGCAAAATTTGGAATGATGTAACCTGTTTCCTC 745
QY 200 SerMetProTrpIleCysGluMetProGluLeuSerProLeuAsp 214
Db 746 AATTATTTTCGGAATTTGTGAAATGTTAGGAATAAATCTCTTTTGAAC 790
RESULT 5
AAx52274
ID AAx52274 standard; DNA; 997 BP.
XX
XX AAx52274;
XX
XX 25-JUN-1999 (first entry)
XX
XX Protein PRO244 cDNA clone DNA35668-1171.
XX
XX Secreted protein; transmembrane protein; human; enterocolitis;
XX Zollinger-Ellison syndrome; gastrointestinal ulceration;
XX congenital microvillus atrophy; skin disease; cell growth;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
XX dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
XX wound healing; tissue repair; ss.
XX
XX Homo sapiens.
XX
XX WO9914328-A2.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-US019330.
XX
XX 17-SEP-1997; 97US-0059113P.
XX
XX 17-SEP-1997; 97US-0059113P.
XX
XX 17-SEP-1997; 97US-0059117P.
XX
XX 17-SEP-1997; 97US-0059119P.
XX
XX 17-SEP-1997; 97US-0059121P.
XX
XX 17-SEP-1997; 97US-0059122P.
XX
XX 17-SEP-1997; 97US-0059184P.
XX
XX 18-SEP-1997; 97US-0059263P.
XX
XX 18-SEP-1997; 97US-0059266P.
XX
XX 15-OCT-1997; 97US-0062125P.
XX
XX 17-OCT-1997; 97US-0062285P.

```


KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
 XX Homo sapiens.
 OS
 XX WO200015796-A2.
 PN
 XX 23-MAR-2000.
 PD
 XX 15-SEP-1999; 99WO-US021090.
 PF
 XX 16-SEP-1998; 98WO-US019330.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 PI Yuan J;
 PI
 DR WPI: 2000-271434/23.
 DR P-PSDB; ADC78689.
 XX
 PT Novel nucleic acids encoding secreted and transmembrane polypeptides with
 PT homology, e.g. to growth and cancer-associated antigens.
 XX
 PS Claim 2; SEQ ID NO 376; 355pp; English.
 XX
 CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
 CC The polypeptides and polynucleotides of the invention may be useful as
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-
 CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
 CC scarring and wound healing, nerve repair, thrombosis, bone and/or
 CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
 CC infertility, premature aging, AIDS, diabetes complications and stroke.
 CC The molecules may also be utilised during gene therapy procedures and
 CC transgenic animal production. The current sequence is that of the human
 CC PRO cDNA of the invention.
 XX
 SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1 41e-72 Length: 997
 Score: 774.00 Matches: 143
 Percent Similarity: 79.07% Conservative: 27
 Best Local Similarity: 66.51% Mismatches: 43
 Query Match: 65.65% Indels: 2
 DB: 3 Gaps: 2

US-10-812-620-2 (1-214) x ADC78688 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPhelysAsnSer 20
 Db 106 ATGAATTCATCTAAATCATCTGAAACACAATGCACAGAGAGGATGCTTC---TCTTCC 162
 Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 Db 163 CAATGTTCTTATGGACTGTTGCTGGGATCCCATCTATTCTCAGTGCCTGTTTCATC 222
 Qy 41 ThrArgCysValValThrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
 Db 223 ACCAGATGTTGTGACATTTGCATCTTTCAAACTGTGATGAGAAAAGTTTCAGCTA 282
 Qy 60 HisArgAsnIleGlyLeuSerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
 Db 283 CCTGAGAATTTTCACAGAGCTCTCTGCTACAAATTATGGATCAGGTTTCAGTCAAGATTCT 342
 Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
 Db 343 TGTCCATTGAACGGGAATATTTCATCCAGCTGCTACTTCTTTCTACTGACACCACT 402

Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
 Db 403 TCCTGGCGTTAAAGTTTAAAGAACTGCTCAGCCATGGGGCTCACCTGGTGTATCAAC 462
 Qy 120 ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysProLysArgLysGluPheTyrIle 139
 Db 463 TCACAGGAGGAGCAGGAATTCCTTTCTTACAAGAAACCTAAATGAGAGAGTTTTTATT 522
 Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
 Db 523 GGACTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 582
 Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
 Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTGGAGGACTGT 642
 Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
 Db 643 GCCACCATGAGAGACTCTTCAAAACCAAGGCAAAATGGAATGATGTAACCTGTTTCCTC 702
 Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
 Db 703 AATTATTTTCGATTGTGAAATGATGGAATAAAATCTTTGAAC 747
 RESULT 7
 AAF72432
 ID AAF72432 standard; cDNA; 997 BP.
 XX
 AC AAF72432;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human PRO244 cDNA.
 XX
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 22-FEB-2000; 2000WO-US004414.
 XX
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US030095.
 PR 16-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Cao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PU, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PW, Wood WI;

```
XX WPI; 2001-081051/09.
DR P-ESDB; AAB80271.
XX
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).
XX
XX Claim 2; Fig 121; 393pp; English.
XX
XX The present sequence is one of sixty one nucleic acids encoding novel
CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding, angiogenesis, ischaemias such as coronary ischaemia,
CC atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid
CC arthritis, multiple sclerosis), infertility, AIDS and diabetes and
CC retinal disorders such as retinitis pigmentosum. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridization
CC probes, and in chromosome and gene mapping
XX
SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1-41e-72 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 4 Gaps: 2

US-10-812-620-2 (1-214) x AAF72432 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACACAAATGCACAGAGAGGATGCTTC---TCITCC 162
Qy 21 GlnValLeuSerThrPheLeuAlaGlyAlaSerLeuPheLeuSerGlyCysPheLeu 40
Db 163 CAATATGTTCTATGGAGCTGTTGCTGGGATCCCATCTCTATTTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTTCGGATCTTCCAACTGCTGATGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAATTTTCACAGAGCTCTCTGCTACAAATATGATGATCAGTTTCAGTCAAGATTGT 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATGAATCGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCATTT 402
Qy 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValLeuAsp 119
Db 403 TCCCTGGGGCTTAAGTTTAAAGAACTGCTCACCCATGGGGGCTCACCCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGGAGGAATTCCTTCTCACAAGAAACCTAAATATGACAGAGATTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTTCAGACCAAGTTGTTCAGGGTTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCCCTGGAGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
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Db 643 GCCACCATGAGAGACTCTTCAAAACCCCAAGGCAAAATTGGAAATGATGAACCTGTTTCCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGGATTTCGAAATGGTAGGAATAAATCCTTTGAAC 747

RESULT 8
AAS45936
ID AAS45936 standard; cDNA; 997 BP.
XX
XX AAS45936;
AC
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX Human DNA encoding PRO polypeptide sequence #12.
DE
XX
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
XX Homo sapiens.
OS
XX
XX WO200168848-A2.
XX
XX 20-SEP-2001.
PD
XX
XX 28-FEB-2001; 2001WO-US006520.
PF
XX
XX 01-MAR-2000; 2000WO-US005601.
PR
XX
XX 02-MAR-2000; 2000WO-US005841.
PR
XX
XX 03-MAR-2000; 2000US-0187202P.
PR
XX
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XX 22-MAY-2000; 2000WO-US014042.
PR
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XX 02-JUN-2000; 2000WO-US015264.
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XX 28-JUL-2000; 2000WO-US020710.
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XX 08-NOV-2000; 2000WO-US030952.
PR
XX
XX 01-DEC-2000; 2000WO-US032878.
PR
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XX 20-DEC-2000; 2000WO-US034956.
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XX (GETH ) GENENTECH INC.
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PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 DR WPI: 2001-602746/68.
 DR P-PSDB; AAU29035.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.

XX PS Claim 2; Fig 23; 774pp; English.

XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 CC primers for PRO polypeptides of the invention. The sequences of the
 CC invention can be used to detect the presence of a tumour in a mammal by
 CC comparing the level of expression of a PRO polypeptide in a test sample
 CC of cells from the animal and a control sample of normal cells, whereby a
 CC higher level of expression in the test sample indicates the presence of a
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders

XX SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,41e-72 Length: 997
 Score: 774.00 Matches: 143
 Percent Similarity: 79.07% Conservative: 27
 Best Local Similarity: 66.54% Mismatches: 43
 Query Match: 65.65% Indels: 2
 DB: 4 Gaps: 2

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 Db 163 CAAATGTTCTTATGGACTTGTGGGATCCCATCTATTCTCAGTGCCTGTTTCATC 222
 QY 41 ThrArgCysValValThrTyrrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
 Db 223 ACCAGATGTTGTGCATTTTCGATCTTCAACCTGTGATGAGAAAAGTTTCAGTGA 282
 QY 60 HisArgAsnIleLysGluLeuSerCysTyrrSerGluAlaSerGlySerValLysAsnCys 79
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 QY 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
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 QY 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrrIle 139
 Db 463 TCACAGGAGGACAGGAATTCCTTCTCCTACAGAAACCTAAATGAGAGAGTTTATTAT 522
 QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
 Db 523 GGACTGTGCAGACAGGTTTTCGAGGGTCAGTGGCAATGGTGGCGGACACACTTTTGACA 582

QY 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
 Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCAACACACATAGCTACCTTGAGGAGCTGT 642
 QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyrr 199
 Db 643 GCCACCATGAGAGACTCTTCAACCCAGGCAAAATTTGAATGATGAACCTGTTTCTCTC 702
 QY 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
 Db 703 AATTATTTTCGATTGTGAAATGCTAGGAATAAATCCTTTTGAAC 747

RESULT 9

ACA60316

ID ACA60316 standard; cDNA; 997 BP.

AC ACA60316;

XX 12-JUN-2003 (first entry)

XX Human cDNA for secreted/transmembrane protein PRO244.

XX Human; ss; gene; secreted protein; transmembrane protein; PRO;
 KW gene therapy; chromosome identification; chromosome marker.

XX Homo sapiens.

XX US2003003530-Al.

XX 02-JAN-2003.

XX 11-JUL-2001; 2001US-00904011.

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 28-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

17-NOV-1997; 97US-0065846P.
 18-NOV-1997; 97US-0065693P.
 21-NOV-1997; 97US-0066112P.
 21-NOV-1997; 97US-0066364P.
 24-NOV-1997; 97US-0066453P.
 24-NOV-1997; 97US-0066466P.
 24-NOV-1997; 97US-0066511P.
 24-NOV-1997; 97US-0066770P.
 24-NOV-1997; 97US-0066772P.
 10-SEP-1998; 98WO-US018824.
 14-SEP-1998; 98WO-US019177.
 16-SEP-1998; 98WO-US019330.
 17-SEP-1998; 98WO-US019437.
 01-DEC-1998; 98WO-US025108.
 08-SEP-1999; 99WO-US020594.
 13-SEP-1999; 99WO-US020944.
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 29-NOV-1999; 99WO-US028214.
 30-NOV-1999; 99WO-US028313.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028564.
 02-DEC-1999; 99WO-US028565.
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 20-DEC-1999; 99WO-US030911.
 20-DEC-1999; 99WO-US030999.
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 11-FEB-2000; 2000WO-US003565.
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 02-MAR-2000; 2000WO-US005841.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 22-MAY-2000; 2000WO-US014042.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 14-AUG-2000; 2000WO-US023328.
 18-SEP-2000; 2000US-00665350.
 (GETH) GENENTECH INC.
 Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 Williams PM, Wood WI;
 WPI; 2003-329602/31.
 P-PSDB; ABU71950.
 New transmembrane polypeptides and nucleic acids encoding the
 polypeptides, useful in gene therapy, in chromosome identification, as
 chromosome markers, in generating probes and in tissue typing.
 Claim 2; Fig 121; 484pp; English.
 The invention relates to an isolated nucleic acid with at least 80%
 nucleic acid sequence identity to a nucleotide sequence encoding one of
 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
 PRO protein/extracellular domain. Also included are a vector comprising
 the PRO nucleic acid, a host cell comprising the vector, producing a PRO
 polypeptide (by culturing the host cell for the expression of the PRO
 polypeptide, and recovering the PRO polypeptide from the cell culture),
 an isolated PRO polypeptide (having at least 80% sequence identity to:
 a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
 acid sequence encoded by a nucleic acid molecule deposited with an ATCC
 number (detailed in the specification); or (c) an extracellular domain of
 a PRO polypeptide or to a PRO polypeptide lacking its associated signal
 peptide), a chimeric molecule comprising a PRO polypeptide of fused to a
 heterologous amino acid sequence, an anti-PRO antibody, detecting a
 PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
 linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and

modulating at least one biological activity of a cell expressing a PRO245
 or PRO1868. Nucleic acids which encode PRO can be used to generate either
 transgenic animals or knock-out animals which may be used in the
 development and screening of therapeutically useful reagents. The nucleic
 acids may also be used in gene therapy, in chromosome identification, as
 chromosome markers, or in generating probes. The PRO polypeptides are
 useful as molecular markers for protein electrophoresis, and the isolated
 nucleic acids may be used for recombinantly expressing those markers. The
 PRO polypeptides and nucleic acids may also be used in tissue typing.
 Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
 affinity purification of PRO from recombinant cell culture or natural
 sources. The present sequence encodes a PRO protein
 SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1-41e-72 Length: 997
 Score: 774.00 Matches: 143
 Percent Similarity: 79.07% Conservative: 27
 Best Local Similarity: 66.51% Mismatches: 43
 Query Match: 65.65% Indels: 2
 DB: Gaps: 2
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 Db 106 ATGAATTCATTAATCATCTGAAACACATGCACAGAGAGGATGCTTC---TCTTCC 162
 Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 Db 163 CAAATGTTCTTATGGACTGTGTGGGATCCCATCTCTATTCTCAGTCGCTTTTCATC 222
 Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
 Db 223 ACCAGATGTGTGTGACATTTCCGATCTCTTCAAACCTGTGTGATGAGAAAAGTTTCAGTA 282
 Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
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 Qy 100 ThrTrpSerSerSerLysAenCysSerAspMetGlyAlaHisLeuValValIleAsp 119
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 Qy 120 ThrGlnGluGlnGluPhePheArgThrLysProLysArgLysGluPheTyrIle 139
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 Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
 Db 703 AATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC 747
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 ID ACA89386 standard; cDNA; 997 BP.
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AC ACA89386;
XX 09-JUL-2003 (first entry)
XX cdNA encoding human PRO polypeptide #12.
XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
KW prostate; rectal; cervical; liver; cancer; TNF-alpha;
KW tumour necrosis factor-alpha; proliferation; differentiation;
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KW arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
KW ss.
XX Homo sapiens.
XX OS
XX US2003036141-A1.
XX PD
XX 20-FEB-2003.
XX 01-JUL-2002; 2002US-00187597.
XX 18-SEP-1997; 97US-0059263P.
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PR 10-AUG-1998; 98US-0096012P.
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PR 17-AUG-1998; 98US-0096766P.

```
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PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
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PR 26-AUG-1998; 98US-0097974P.
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PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100684P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
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PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
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PR 23-SEP-1998; 98US-0101475P.
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PR 24-SEP-1998; 98US-0101738P.
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PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 25-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Alignment Scores:
Pred. No.: 1.41e-72
Score: 774.00
Percent Similarity: 79.07%
Best Local Similarity: 66.51%
Query Match: 65.65%
DB: 8

US-10-812-620-2 (1-214) x ACA89386 (1-997)

Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTTCATCTAAATCATCTGAACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTAUGAGATGTTGCTGGGATCCCATCTATTTCTCACTGCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AenLeuGlnPro 59
Db 106 ATGAATTTCATCTAAATCATCTGAACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162

223 ACCAGATGTTGTGACATTTTCGATCTTTCAACCTGTGATGAGAAAAAGTTTCAGCTA 282
60 HisArgAenIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAenCys 79
283 CCTGAGAAATTTACAGAGCTCTCTCTGTACAAATTTATGGATCAGGTTTCAGTCAAGATTGT 342
80 CysProLeuAenTrpLysHisTyArgGlnSerSerCysTySerPhePheSerThrThrLeu 99
343 TGTCCATTTGAATGGGAATATTTTCAATCCAGCTGCTACTTCTTTTCTACTGACACCATTT 402
100 ThrTrpSerSerSerLeuLysAenCysSerAenMetGlyAlaHisLeuValValIleAen 119
403 TCTGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC 462
120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyIle 139
463 TCACAGGAGGAGCAGGAATTTCTTCTACAGAAACCTTAAATGAGAGAGATTTTATT 522
140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
523 GGACTGTGACAGCAGGTTGTCGAGGGTTCAGTGGCAATGGGTGGACGCGCACCTTTGACA 582
160 GluSerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAenCys 179
583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGCCCAACAACTAGCTACCTCGGAGGACTGT 642
180 AlaThrIleArgAspSerSerAenSerArgLysAenTrpAenAspIleProCysPheTy 199
643 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATTTGGAATGATGATTAACCTGTTCTC 702
200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAen 214
703 AATTATTTTCGGATTTGCGAATGCTAGGAATAAATCCTTTTGAAC 747

RESULT 11
ACA73396
ID ACA73396 standard; cDNA; 997 BP.
XX AC ACA73396;
XX DT 01-JUL-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) cDNA #12.
XX KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
XX KW proliferation; differentiation; chondrocyte cells;
XX KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX OS Homo sapiens.
XX PN US2003036146-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00187603.
XX PR 26-JUN-1998; 98US-00105413.
XX PR 16-SEP-1998; 98WO-US019330.
XX PR 07-OCT-1998; 98US-00168978.
XX PR 07-OCT-1998; 98WO-US021141.
XX PR 06-NOV-1998; 98US-00187368.
XX PR 01-DEC-1998; 98WO-US025108.
XX PR 07-DEC-1998; 98US-00202054.
XX PR 03-MAR-1999; 99US-00254311.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 14-MAY-1999; 99US-00311832.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 25-AUG-1999; 99US-00380137.
XX PR 25-AUG-1999; 99US-00380138.
XX PR 25-AUG-1999; 99US-00380139.
XX PR 25-AUG-1999; 99US-00380142.
XX PR 01-SEP-1999; 99WO-US020111.
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PR 15-SEP-1999; 99WO-US021090.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028551.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004411.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US033709.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 08-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 08-SEP-2000; 2000US-00665350.
 PR 18-SEP-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941992.
 PR 29-AUG-2001; 2001US-00947099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.
 (GETH) GENENTECH INC.
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-332034/31.
 DR P-PSDB; ABUS6204.
 XX Three hundred and five nucleic acids encoding PRO polypeptides, useful in
 PT gene therapy, chromosome identification, tissue typing, and for detecting
 PT the presence of tumor in a mammal.
 XX Claim 2; Fig 23; 707pp; English.
 CC The invention relates to three hundred and five nucleic acids encoding
 CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to
 CC them, or encoding a PRO polypeptide lacking its associated signal peptide
 CC or an extracellular domain of the PRO polypeptide, with or lacking its
 CC associated signal peptide. Also included are the encoded PRO proteins,
 CC PRO expression vectors, host cells transformed with the vector (used to
 CC produce PRO proteins), a chimeric molecule comprising the PRO
 CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
 CC antibody, a method for stimulating the release of tumor necrosis factor
 CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,

CC PRO827, PRO791, PRO131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or
 CC PRO4333), a method for stimulating the proliferation or differentiation
 CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
 CC a method for detecting the presence of tumor in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences cited
 CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
 CC as hybridisation probes in chromosome and gene mapping, or in generating
 CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
 CC polypeptides, in assays to identify other proteins or molecules involved
 CC in a binding reaction, to generate transgenic animals or knockout
 CC animals, which in turn are useful in the development and screening of
 CC therapeutically useful reagents, for chromosome identification, and
 CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
 CC useful for detecting the presence of a tumour in a mammal, stimulating the
 CC proliferation or differentiation of chondrocyte cells, stimulating the
 CC release of tumour necrosis factor-alpha from human blood, in gene
 CC therapy, or as molecular weight markers for protein electrophoresis
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
 CC PRO, or for the affinity purification of PRO from recombinant cell
 CC culture or natural sources. The present sequence is a cDNA encoding a PRO
 CC protein
 XX
 SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.41e-72 Length: 997
 Score: 774.00 Matches: 143
 Percent Similarity: 79.07% Conservative: 27
 Best Local Similarity: 66.51% Mismatches: 43
 Query Match: 65.65% Indels: 2
 DB: 8 Gaps: 2
 US-10-812-620-2 (1-214) x ACA73396 (1-997)
 QY 1 MetAenSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAenSer 20
 DB 106 ATGAATTCATCTAATCATCTGAAACACAATGCACAGAGAGAGATGCTTC---TCTTCC 162
 QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 DB 163 CAATGTTCTTATGGACTGTTGCTGGGATCCCATCTCTTCTCAGTGCCTGTTTCATC 222
 QY 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AenLeuGlnPro 59
 DB 223 ACCAGATGTGTGTGACATTTTCGATCTTTCAAAACCTGTGATGAGAAAAGTTTCAGCTA 282
 QY 60 HisArgAenIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAenCys 79
 DB 283 CTGGAATTTTCACAGAGCTCTCTGCTACAAATATGATGATCAGGTTCAGTCAAGAAATTGT 342
 QY 80 CysProLeuAenTrpLysHisTyArgGlnSerSerCysTySerPhePheSerThrThrLeu 99
 DB 343 TGTCCATTGAACATGGGAATATTTTCAATCCAGCTGCTACTCTTCTTCTTACTGACACCAT 402
 QY 100 ThrTrpSerSerSerLeuLysAenCysSerSerMetGlyAlaHisLeuValValIleAsp 119
 DB 403 TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTATCAAC 462
 QY 120 ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyIle 139
 DB 463 TCACAGGAGGACAGGAATTTCTTCTTACAGAAACCTAAATGAGAGAGATTTTATT 522
 QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
 DB 523 GGACTGTCAGACAGAGTTGTTCAGGGTTCAGTGGCAATGGTGGAGCGGCACACCTTTGACA 582
 QY 160 GluSerLeuSerPheTrpAspAlaGlyGlnProAenAenIleValLeuValGluAspCys 179
 DB 583 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGGCCCAACAACATAGCTACCTGGAGACTGT 642
 QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAenTrpAenAspIleProCysPheTy 199

QY 21 GinValLeuSerThrPheAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheile 40
 Db 163 CAAATGTTCTTATGGACTTCTGGATCCCATCTTATCTCAGTCCCTGTTTCATC 222
 QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
 Db 223 ACCAGATGTGTGTGACATTCGCATCTTTCAAACTGTGTGATGAGAAAAAGTTTCAGCTA 282
 QY 60 HisArgAsnIleGlySerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
 Db 283 CTTGAGAAATTTACAGAGCTCTCTGCTACAAATATGGATCAGGTTTCAGTCAAGAAATGT 342
 QY 80 CysProLeuAsnTriPheHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
 Db 343 TGTCCATGAACTGGGAATATTTCAATCCAGCTGCTACTTCTTTCTACTGACCAAT 402
 QY 100 ThrTriPheSerSerSerLeuIysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
 Db 403 TCCTGGCGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGTATCAAC 462
 QY 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProIysArgLysGluPheTyrIle 139
 Db 463 TCACAGGAGGACGAGAAATTCCTTCTCCTACAGAAACCTAAATGAGAGAGTTTTTAT 522
 QY 140 GlyLeuThrAspGlnValValGluGlyGlnTyrGlnTyrValAspAspThrProPheThr 159
 Db 523 GGAATGTCACACAGGTTGTGAGGTCAGTGGCAATGGTGGACGGCACCTTTTGACA 582
 QY 160 GluSerLeuSerPheThrAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
 Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCAACACATAGCTACCTCGGAGGACTGT 642
 QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTriPheAsnIleProCysPheTyr 199
 Db 643 GCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATTTGAATCATGTACCTGTTTCTCTC 702
 QY 200 SerMetProTriPheCysGluMetProGluIleSerProLeuAsp 214
 Db 703 AATTATTTTCGGATTTGTGAAATGGTAGGAATAAAATCTTTTGAAC 747
 RESULT 13
 ID ACA66545 standard; cDNA; 997 BP.
 XX ACA66545;
 AC ACA66545;
 XX
 DT 23-JUN-2003 (first entry)
 XX cDNA encoding human PRO protein #12.
 DE Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
 KW liver; PRO; gene therapy; gene; ss.
 XX Homo sapiens.
 OS
 XX
 PN US2003036137-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 27-JUN-2002; 2002US-00184640.
 XX
 PR 26-JUN-1998; 98US-00105413.
 PR 16-SEP-1998; 98WO-US019330.
 PR 07-OCT-1998; 98US-00168978.
 PR 06-OCT-1998; 98WO-US021141.
 PR 06-NOV-1998; 98US-00187368.
 PR 01-DEC-1998; 98WO-US025108.
 PR 07-DEC-1998; 98US-00202054.
 PR 03-MAR-1999; 99US-00254311.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.

PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028551.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941992.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-342038/32.
 P-PSDB; ABU00445.

Three hundred and five nucleic acids encoding secreted and transmembrane
 PRO polypeptides, useful for the diagnosis, prevention and/or treatment
 of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
 cervical or liver tumors.

Claim 2; Fig 23; 708pp; English.

The invention relates to three hundred and five nucleic acids encoding
 PRO polypeptides (secreted and transmembrane). Methods and compositions
 of the present invention are useful for the diagnosis, prevention and/or
 treatment of tumours, such as adrenal, lung, colon, breast, prostate, rectal,

CC rectal, cervical or liver tumours. The PRO polypeptides are also useful
CC as molecular weight markers, or for chromosome identification. The PRO
CC genes are useful as hybridisation probes, or for screening libraries of
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. The present
CC sequence represents a cDNA encoding a human PRO polypeptide of the
CC invention

XX Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.41e-72	Length:	997
Score:	774.00	Matches:	143
Percent Similarity:	79.07%	Conservative:	27
Best Local Similarity:	66.51%	Mismatches:	43
Query Match:	65.65%	Indels:	2
DB:	8	Gaps:	2

US-10-812-620-2 (1-214) x ACA66545 (1-997)

Qy	1	MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer	20
Db	106	ATGAATTCATCTAATCATCTGAAACACATGACAGAGAGGATGCTTC---TCTTCC	162
Qy	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
Db	163	CAATGTTCTTATGGACTTCTGCTGGATCCCATCTCTATTTCTCAGTGCCTGTTTCATC	222
Qy	41	ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro	59
Db	223	ACCAGATGTTGTGACATTTCCGATCTTTCAACACCTGTGATGAGAAAGATTTCAGCTA	282
Qy	60	HisArgAsnIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAsnCys	79
Db	283	CCTGAGATTTCACAGAGCTCTCTGCTACAAATATGATCAGGTTTCTCAGTCAAGATTGT	342
Qy	80	CysProLeuAsnTrpLysHisTyGlnSerSerCysTyPhePheSerThrThrLeu	99
Db	343	TGTCATTTGAATCGGAATATTTTCAATCCAGCTGCTACTTCTTTCTTCTGACACCAT	402
Qy	100	ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp	119
Db	403	TCCTGGGGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGCTCACCTGGTGGTTTATCAAC	462
Qy	120	ThrGlnGluGlnGluPhePheArgThrLysProLysArgLysGluPheTyIle	139
Db	463	TCACAGAGGAGCAGGAATTCCTTCTTACAGAAACCTAAATGACAGAGATTTTATT	522
Qy	140	GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr	159
Db	523	GGACTGTACAGACCAAGTTGCGAGGTCAGTGGCAATGGGTGGACGCACACCTTTTGACA	582
Qy	160	GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys	179
Db	583	AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTCTGGAGACTGT	642
Qy	180	AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr	199
Db	643	GCCACCATGAGAGACTCTTCAACCCCAAGGAAATTTGGAATGATGTAACCTGTTTCTTC	702
Qy	200	SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp	214
Db	703	AATTATTTCGATTTGTGAAATGGTAGGAATAAATCCTTTGAC	747

RESULT 14

ACD07717
ID ACD07717 standard; DNA; 997 BP.
XX
AC ACD07717;
XX
DT 07-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PCR primer #151.

XX	Human; secreted and transmembrane protein; PRO; pharmaceutical;
KW	diagnostic; biosensor; bioindicator; Parkinson's disease;
KW	Alzheimer's disease; inflammation; nephritis; wound healing;
KW	nerve repair; collateral blood vessel formation; cancer;
KW	colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
KW	cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
KW	scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
KW	infertility; gene therapy; PCR; primer; ss.
XX	Homo sapiens.
OS	US2002197671-A1.
PN	26-DEC-2002.
XX	17-JUL-2001; 2001US-00907824.
PR	17-SEP-1997; 97US-0059113P.
PR	17-SEP-1997; 97US-0059115P.
PR	17-SEP-1997; 97US-0059117P.
PR	17-SEP-1997; 97US-0059119P.
PR	17-SEP-1997; 97US-0059121P.
PR	17-SEP-1997; 97US-0059122P.
PR	17-SEP-1997; 97US-0059184P.
PR	18-SEP-1997; 97US-0059263P.
PR	18-SEP-1997; 97US-0059266P.
PR	15-OCT-1997; 97US-0062125P.
PR	17-OCT-1997; 97US-0062285P.
PR	17-OCT-1997; 97US-0062287P.
PR	21-OCT-1997; 97US-0063486P.
PR	24-OCT-1997; 97US-0062814P.
PR	24-OCT-1997; 97US-0062816P.
PR	24-OCT-1997; 97US-0063045P.
PR	24-OCT-1997; 97US-0063120P.
PR	24-OCT-1997; 97US-0063121P.
PR	24-OCT-1997; 97US-0063127P.
PR	24-OCT-1997; 97US-0063128P.
PR	27-OCT-1997; 97US-0063327P.
PR	27-OCT-1997; 97US-0063329P.
PR	28-OCT-1997; 97US-0063341P.
PR	28-OCT-1997; 97US-0063342P.
PR	28-OCT-1997; 97US-0063344P.
PR	28-OCT-1997; 97US-0063349P.
PR	28-OCT-1997; 97US-0063550P.
PR	28-OCT-1997; 97US-0063564P.
PR	29-OCT-1997; 97US-0063435P.
PR	29-OCT-1997; 97US-0063704P.
PR	29-OCT-1997; 97US-0063732P.
PR	29-OCT-1997; 97US-0063734P.
PR	29-OCT-1997; 97US-0063735P.
PR	29-OCT-1997; 97US-0063738P.
PR	31-OCT-1997; 97US-0064215P.
PR	31-OCT-1997; 97US-0064103P.
PR	03-NOV-1997; 97US-0064248P.
PR	07-NOV-1997; 97US-0064809P.
PR	12-NOV-1997; 97US-0065186P.
PR	17-NOV-1997; 97US-0065846P.
PR	18-NOV-1997; 97US-0065693P.
PR	21-NOV-1997; 97US-0066120P.
PR	21-NOV-1997; 97US-0066364P.
PR	24-NOV-1997; 97US-0066453P.
PR	24-NOV-1997; 97US-0066466P.
PR	24-NOV-1997; 97US-0066511P.
PR	24-NOV-1997; 97US-0066770P.
PR	24-NOV-1997; 97US-0066772P.
PR	10-SEP-1998; 98WO-US018824.
PR	14-SEP-1998; 98WO-US019177.
PR	16-SEP-1998; 98WO-US019330.
PR	17-SEP-1998; 98WO-US019437.
PR	01-DEC-1998; 98WO-US025108.
PR	08-SEP-1999; 99WO-US020594.

XX 26-JUN-2002; 2002US-00183006.
PF 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-00632250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-00631120P.
PR 24-OCT-1997; 97US-00631121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
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PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069435P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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PR 20-MAR-1998; 98US-0078886P.
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PR 27-MAR-1998; 98US-0079664P.
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PR 22-MAY-1998; 98US-0086332P.
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PR 10-JUN-1998; 98US-0088825P.
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Job time : 547 secs

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Score:	774.00	Matches:	143
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DB:	8	Gaps:	2

US-10-812-620-2 (1-214) x ACF20120 (1-997)

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DB	106	ATGAATTCATCTAAATCATCTGAAACAATGCACAGAGAGGATGCTTC---TCTTCC	162
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DB	163	CAAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCCTATTCTCAGTGCGCTTTTCATC	222
QY	41	ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro	59
DB	223	ACCAGATGTGTTGTGACATTTTCGATCTTTCAAACTGTGATGAGAAAAAGTTTCAGTCA	282
QY	60	HisArgAsnIleGlyGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys	79
DB	283	CCTGAGAATTTCCACAGAGCTCTCTCGCTACCAATTATGGATCAGGTTCACTCAAGAAATGT	342
QY	80	CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu	99
DB	343	TGTCCATTGAATCGGGAATATTTCATTCACAGCTGCTACTTCTTTCTACTGCACCAAT	402
QY	100	ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp	119
DB	403	TCTTGGCGCTTAAGTTTAAGAAACTGCTCAGCCATATGGGGCTCACTCGTGGTATTCAAC	462
QY	120	ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle	139
DB	463	TCACAGGAGGACAGGAATTCCTTTCCCTACAGAAACCTAAATGAGAGAGATTTTTATT	522
QY	140	GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr	159

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2005, 12:24:29 ; Search time 3168 Seconds
(without alignments)
2571.261 Million cell updates/sec

Title: US-10-812-620-2

Perfect score: 1179

Sequence: 1 MNSTKSPASHHTRGCFKNS.....IPCFYMPWICEMPEISPLD 214

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
	Ygapop 10.0 , Ygapext 0.5
	Fgapop 6.0 , Fgapext 7.0
	Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2 1/US10812620/runat_07062005_124337_3256/app query faeta_1.391
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-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

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9:	gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1116	94.7	2233	3 AK089286	Mus muscu
2	1002.5	85.0	660	2 BE292395	601057892
3	961.5	81.6	717	6 BY743963	BY743963
4	949	80.5	644	4 BG080418	H3053D08-
5	944.5	80.1	667	6 BY747840	BY747840
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7	942	79.9	674	6 BY744630	BY744630
8	936	79.4	655	6 BY749084	BY749084
9	928	78.7	666	6 BY747821	BY747821

10	920.5	78.1	728	6	BY742764	BY742764	
11	917	77.8	645	6	BY743467	BY743467	
12	905	76.8	643	6	BY743813	BY743813	
13	808	68.5	671	6	BY749488	BY749488	
14	735.5	62.4	1032	2	BE311916	601143328	
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C	20	649.5	55.1	718	6	CB528932	UI-H-FT2-
C	21	637	54.0	614	6	CB474859	in909 D09
C	22	631	53.5	618	6	CB453374	708350 MA
C	23	625.5	53.1	738	5	BQ004812	UI-H-E10-
C	24	623	52.8	691	6	CD742945	UI-H-FT1-
C	25	608	51.6	473	2	BB860060	BB860060
C	26	606	51.4	645	6	CD368203	UI-H-FT1-
C	27	602	51.1	404	5	BY201224	BY201224
C	28	602	51.1	405	5	BY161340	BY161340
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C	31	564	47.8	358	5	BY200082	BY200082
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C	37	513	43.5	361	5	BY203558	BY203558
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C	40	510	43.3	415	2	BB850328	BB850328
C	41	505	42.8	398	5	BY160494	BY160494
C	42	493	41.8	352	5	BY184536	BY184536
C	43	491	41.6	387	5	BY155120	BY155120
C	44	489	41.5	393	5	BY161254	BY161254
C	45	489	41.5	393	5	BY167126	BY167126

ALIGNMENTS

RESULT 1	AK089286	2233 bp	mrna	linear	HTC 03-APR-2004
LOCUS	Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN				
DEFINITION	full-length enriched library, clone:F73001C01 product:c-type				
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	superfamily member 9, full insert sequence.				
ACCESSION	AK089286				
VERSION	AK089286.1	GI:26105181			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	1				
	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				
	Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
	Normalization and subtraction of cap-trapper-selected cDNAs to				
	prepare full-length cDNA libraries for rapid discovery of new genes				
	Genome Res. 10 (10), 1617-1630 (2000)				
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REFERENCE	3				
	Shibata, K., Itoh, H., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,				
	Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,				
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,				
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,				

Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

4

11076861

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2233)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/, tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/

Location/Qualifiers

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misc_feature

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1116.00 Matches: 211

88.66% Conservativeness: 0

88.66% Mismatches: 3

Best Local Similarity:

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

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Query Match: 94.66% Indels: 25
DB: 3 Gaps: 1

US-10-812-620-2 (1-214) x AK089286 (1-2233)

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DB 124 ATGAATTCAACCAATCGCTGCATCCACACACAGAGAGAGAGATGCTTTCAAAATCC 183

QY 21 GlnValLeuSerThrThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40

DB 184 CAAAGTGTCTCTCTGACGATAGCCGGGCGCTCCATCTCTCTCTCTCTCTCTCTCTCTCT 243

QY 41 ThrArgCysValValThrThrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60

DB 244 ACCAGATGTGTCGTAACATATCGCTGCTCTCAAAATTCGGGCAGAACTTACAGGCACAT 303

QY 61 ArgAsnIleLysGluLeuSerCysTyrSerGluAlaSer----- 73

DB 304 AGAATATTAAGGAGCTTTCTGTCTACAGTGAGGCATCAGGTATAACCATCTGCAGCACA 363

QY 74 -----GlySerVal 76

DB 364 CAGAATCATTTAGCAAAAGTTTCTGGGCAATGTCTGAAGCCTTTCTCTCTCTTAGGTTTCAGTC 423

QY 77 LysAenCysCysProLeuAenTrpLysHisIleThrGlnSerSerCysTyrPhePheSerThr 96

DB 424 AAGAATTTGCTGTCTTGAACATGGAACATTAATCAATCTAGTTGTATATTTTTTCTCTACG 483

QY 97 ThrThrLeuThrTrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuVal 116

DB 484 ACAACCTTGACCTGTGTCATCAAG-TTAAAGAAATTCCTCAGACATGGGGCTCACCTGGTG 542

QY 117 ValIleAspThrGlnGluGlnGluPheArgThrLysProLysArgLysGlu 136

DB 543 GTTATCGACACACAG 602

QY 137 PheTyrIleGlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThr 156

DB 603 TTTTATATTGGACTGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 662

QY 157 PropheThrGluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuVal 176

DB 663 CTTTTCACAGAGTCTCTGAGCTTCTGGGATGCTGGGAGCCCAACAATATAGTTTGGTG 722

QY 177 GluAspCysAlaThrIleArgAspSerSerAenSerArgLysAenTrpAsnAspIlePro 196

DB 723 GAGGAGCTGTGCCACCATTAAGGAGACTCTTCAAACTCCAGGAAGATCTGGAATGATATACCC 782

QY 197 CysPheTyrSerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214

DB 783 TGTTTCTACAGTATGCTTGGATTGTGAGATGCCAGAAATTAAGTCTCTCTGAC 836

RESULT 2

BE292395

LOCUS

601057892F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3158063 5',

DEFINITION

mRNA sequence.

ACCESSION

BE292395

VERSION

BE292395.1 GI:9174758

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NIH-MGC http://mgi.nci.nih.gov/.

REFERENCE

1 (bases 1 to 660)

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.

FEATURES
SOURCE

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Site 2: NCI; Cloned unidirectionally. Prim
Library constructed by Life Technologies. In
providing samples: Jeffrey Green, M.D. NTH"

```

REFERENCE

AUTHORS

1. (pages 1 to 717)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonberger, C., Gotobori, T., Balderelli, R., Hill, D. P., Bult, C.

US-10-812-620-2 (1-214) x BE292395 (1-660)

FORM	COMMENT
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Tel: 81-45-503-9222
Fax: 81-45-503-9216

Fax: 81-45-503-9216
 Email: genome-resesegc.riken.jp, URL: <http://genome.resc.riken.jp/>
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashigume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source Location/Qualifiers
1..717
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I830025C13"
/tissue_type="bone marrow"
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/clone_lib="RIKEN full-length enriched, bone marrow macrophage"

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Alignment Scores:
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Score: 961.50 Matches: 187
Percent Similarity: 95.94% Conservative: 2
Best Local Similarity: 94.92% Mismatches: 7
Query Match: 81.55% Indels: 3
DB: 6 Gaps: 1

US-10-812-620-2 (1-214) x BY743963 (1-717)

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DB 123 ATGAATTTCACCAAAATCGCTGCATCCACCACACAGAGAGAGATGCTTCAAAAACCTCC 182
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
DB 183 CAAGTGTCTCTCTGGACGATAGCCGGGGCTCCATCTGTTTCTAGTGGCTTTTCATC 242
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
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QY 101 TrpSerSerSerLeuIysAsnCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
DB 423 TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGGCTCACCTGGTGTATCGACACA 482
QY 121 GlnGluGlnGlnGluPheIleuPheArgThrLysProIysArgIysGluPheTyrIleGly 140
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DB 543 CTGACAGACAGGTGGTGGAGGTTCAGTGGCAATGGGTGGATGATACCTTTTCAGAG 602
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QY 181 ThrIleArgAspSerSerAsnSerArgIysAsnTrpAsnAspIleProCys 197
DB 661 ACCATAGGAGACTCTTCAACTCCCGAGAA---CTGGATGATATACCTGT 708

RESULT 4
BG080418

LOCUS BG080418 644 bp mRNA linear EST 17-DEC-2003
DEFINITION H3053D08-5 N1A Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3053D08 5', mRNA sequence.
ACCESSION BG080418
VERSION BG080418.2 GI:40014148
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 644)
AUTHORS Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H.
TITLE Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
MEDLINE 20381348
PUBMED 10922068
COMMENT On Jan 26, 2001 this sequence version replaced gi:12562986.
Other ESTs: H3053D08-3
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@gsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
Plate: H3053 row: D column: 08
Seg primer: -21M13 Reverse
High quality sequence stop: 644
POLYA=No.
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/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN

Alignment Scores:

Pred. No.: 1.25e-93 Length: 644
 Score: 949.00 Matches: 178
 Percent Similarity: 99.44% Conservative: 0
 Best Local Similarity: 99.44% Mismatches: 1
 Query Match: 80.49% Indels: 1
 DB: 4 Gaps: 0

US-10-812-620-2 (1-214) x BG080418 (1-644)

QY 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
 DB 109 ATGAATTCACCAATCGCTCCATCCACACAGAGAGGATGCTTCAAAAATCC 168
 QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 DB 169 CAAGTGCTCTCTGGAGCATAGCCGGGCTCCATCTGTTCTCAGTGGCTTTTATC 228
 QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAenLeuGlnProHis 60
 DB 229 ACCAGATGTGTCGTAACATATCGCAGCTCTCAAAATTTCCGGCAGAACTTACAGCCACAT 288
 QY 61 ArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCysCys 80
 DB 289 AGAAATATTAAAGGAGCTTTCTCTGCTACAGTACGAGCATCAGGTTTCAGTCAAGAAATTCGCTGT 348
 QY 81 ProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr 100
 DB 349 CCTTTGAACTGGAAACATATCAATCTAGTTGTTATTTTCTCTACGACAACTTGACC 408
 QY 101 TrpSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
 DB 409 TGGTCATCAAGTTTAAAGAAATTCCTCAGACATGGGGCTCACCTGGTGGTTATCGACACA 468
 QY 121 GlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
 DB 469 CAGGAAGACGAGGAATTCCTTTTCGACAAACCTTAAAGGAAGAGATTTTATATTGGA 528
 QY 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
 DB 529 CTGACAGACCCAGGTGGTGGAGGTTCAGTGGCAATGGGTGGATGATACACCTTTTACAGAG 588
 QY 161 SerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAspCys 179
 DB 589 TCCCTGAGCTTCTGGGATGCTGGGAGCCAC-AATATAGTTTTTGGTGGAGGACTGT 644

RESULT 5

BY747840 667 bp mRNA linear EST 17-DEC-2002
 LOCUS BY747840.1 GI:27176343
 DEFINITION dendritic cells Mus musculus cDNA clone F630012G18 5', mRNA sequence.

ACCESSION

BY747840
 VERSION BY747840.1 GI:27176343
 KEYWORDS EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 667)

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yananaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., But, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaj, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L.G., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayateu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

MEDLINE

22354683

PUBMED

12466851

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopaedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

1. 667
 /organism="Mus musculus"
 /mol_type="mRNA"
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 /db_xref="taxon:10090"
 /clone="F630012G18"
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ORIGIN

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 Score: 944.50 Matches: 185

Percent Similarity:	95.92%	Conservative:	3
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US-10-812-620-2 (1-214) x BY747840 (1-667)			
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DB	135	CAAGTGCTCTCTGGACGATACCGGGGCTCCATCTGTTCTCAGTGGCTGTTCATC	194
QY	41	ThrArgCysValValThrTrpArgSerSerGlnIleSerGlyClnAenLeuGlnProHis	60
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QY	61	ArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCysCys	80
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DB	315	CTTTGAACCTGGAACATATCAATCTAGTTGTATTTTCTTACGACACCTTGACC	374
QY	101	TrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValLleAspThr	120
DB	375	TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGGCTCACCTGGTGGTTATCGACACA	434
QY	121	GlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly	140
DB	435	CAGGAAGACGAGAAATTCCTTTTCGCACAAACCTTANAAGGAAGAGTTTATATGGA	494
QY	141	LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu	160
DB	495	CTGCACAGACAGGTGGTGAGGGTCACTGNCATGGTGGATGATACACCTTTCACAGAG	554
QY	161	SerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAspCysAla	180
DB	555	TCCTCGAGCTTCGGGATGCTGNAGAGCCCA-CATATAGTTTGGTGGAGGACTGTGCC	613
QY	181	ThrIleArgAspSerSerAenSerArgLysAenTrpAsnAspIlePro	196
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AK036493			
LOCUS	AK036493 4017 bp mRNA linear HTC 03-APR-2004		
DEFINITION	Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830118H07 product:c-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, full insert sequence.		
ACCESSION	AK036493		
VERSION	AK036493.1 GI:26085261		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
TITLE	Genome Res. 10 (10), 1617-1630 (2000)		
JOURNAL			
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, H., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
AUTHORS	Functional annotation of a full-length mouse cDNA collection		
TITLE	Nature 409, 685-690 (2001)		
JOURNAL	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
TITLE	Nature 420, 563-573 (2002)		
JOURNAL	6 (bases 1 to 4017)		
REFERENCE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, D., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, Y., Tanaka, T., Tomaru, A., Toyata, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.		
FEATURES	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.		
source	Location/Qualifiers		
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	/organism="Mus musculus"		
	/mol_type="mRNA"		
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	/db_xref="FANTOM DB:9830118H07"		
	/db_xref="taxon:10090"		
	/clone="9830118H07"		
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Db	2644	AGCTCTCAAAATTCGGGCGAGAACTTACAGCCACATAGAAATATTAAGGAGCTTTCCTGCG	-----	2703		
QY	69	TyrSerGluAlaSerGlySerValIysAsnCysCysProLeuAsnTrpLysHisTyrGln	-----	88		
Db	2704	TACAGTGAGGCATCAGGTTCACTCAGAAATTCGTCTTGAAGTGAACATATATCAA	-----	2763		
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ACCESSION	BY744630					
VERSION	BY744630.1	GI:27171386				
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SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
	1 (bases 1 to 674)					
	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,					
	Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,					
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Nature 420, 563-573 (2002)	
22354683	
12466851	
Contact: Yoshihide Hayashizaki	
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute	
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Fax: 81-45-503-9216	
Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/	
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Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.	
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.	
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FEATURES	
source	

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

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FEATURES
Source
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US-10-812-620-2 (1-214) x BY744630 (1-674)

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RESULT 8

BY749084

LOCUS

DEFINITION

BY749084 655 bp mRNA linear EST 17-DEC-2002
dendritic cells Mus musculus cDNA clone F630224E05 5', mRNA

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 655)

REFERENCE

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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COMMENT

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The Institute of Physical and Chemical Research (RIKEN)
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Division of Experimental Animal Research in Riken contributed to
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Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.

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FEATURES

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ORIGIN

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DEFINITION				
BY747821 RIKEN full-length enriched, NOD-derived CD11c +ve				
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BY747821				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Mus musculus (house mouse)				
REFERENCE				
AUTHORS				
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
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Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES
source

Location/Qualifiers
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/clone="F630011J05"
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QY	21	GlnValLeuSerThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
DB	184	CAAGTGTCTCTCTGGACGATAGCCGGGCTCCATCTCTTCTCAGTGGCTGTTTCATC	243
QY	41	ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGlnAenLeuGlnProHis	60
DB	244	ACCAGATGTGTGTAACATATCGCAGCTCTCAAAATTCGGGCAACAATTACAGCCACAT	303
QY	61	ArgAenIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAenCysCys	80
DB	304	AGAATAATTAGGAGCTTCTCTGCTACAGTGAGGCATCAGTTCAAGAAATTGCTGT	363
QY	81	ProLeuAenTrpLysHisTyArgSerCysTySerPhePheSerThrThrThrLeuThr	100
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DEFINITION	BY742764	musculus cDNA clone G530005P16 5', mRNA sequence.	
ACCESSION	BY742764		
VERSION	BY742764.1	GI:27168500	
KEYWORDS	EST.		
SOURCE	Mus musculus		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Mateuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takanaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,		
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encyclopedia: real-time sequence clustering for construction of a			
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)			
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Genomic Sciences Center and Genome Science Laboratory in Riken.			
Division of Experimental Animal Research in Riken contributed to			
prepare mouse tissues.			
Tissues were provided by David A. Hume (Dept. of Biochemistry			
and Microbiology/Parasitology Institute for Molecular Bioscience			
University of Queensland Brisbane, Q 4072 Australia) whose			
assistance we gratefully acknowledge.			
Please visit our web site (http://genome.gsc.riken.go.jp) for			
further details.			
FEATURES	Location/Qualifiers		
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Alignment Scores:			
Pred. No.:	2.03e-90	Length:	728
Score:	920.50	Matches:	179
Percent Similarity:	83.64%	Conservative:	0
Best Local Similarity:	83.64%	Mismatches:	6
Query Match:	78.07%	Indels:	31
DB:	6	Gaps:	1

US-10-812-620-2 (1-214) x BY742764 (1-728)

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RESULT 11

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DEFINITION musculus cDNA clone 1830011F16 5', mRNA sequence.
ACCESSION BY743467
VERSION BY743467.1 GI:27169524
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 645)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Bruscia, V.,
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragan, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
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Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata, K.,
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PUBMED 12468851
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FEATURES
source 1. 645
/organism="Mus musculus"
/mol_type="mRNA"
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ORIGIN

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Pred. No.: 917.00 Matches: 169
Score: 98.83% Conservative: 0
Percent Similarity:

Best Local Similarity:	98.83%	Mismatches:	2
Query Match:	77.78%	Indels:	0
DB:	6	Gaps:	0
US-10-812-620-2 (1-214) x BY743467 (1-645)			
QY	1	MetAsnSerThrIysSerProAlaSerHisThrGluArgGlyCysPheIysAsnSer	20
DB	124	ATGAATTCACCAAAATCGCTGCATCCACACACAGAGAGAGGATGCTTCAAAACTCC	183
QY	21	GlnValIeuSerTrpThrIleAlaGlyAlaSerIleIeuPheIeuSerGlyCysPheIle	40
DB	184	CAAGTGCTCTCCGGACGATAGCGGGGCTCCATCCTGTCTCAGTGGCTGTTCATC	243
QY	41	ThrArgCysValValThrTrpArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis	60
DB	244	ACCAGATGTGCTGTAACATATCGACGCTTCAAAATTCGGGACGAGACTTACAGGCACAT	303
QY	61	ArgAsnIleGlyGluLeuSerCysTrpSerGluAlaSerGlySerValIysAsnCysCys	80
DB	304	AGAAATATTAAAGAGCTTCTCTGCTACAGTGAGGCATCAGGTTTCAGTCAAGAATTGCTGT	363
QY	81	ProLeuAsnTrpIysHisTrpGlnSerSerCysTrpPhePheSerThrThrThrLeuThr	100
DB	364	CCTTTGAACGTGGAACATATATCAATCTAGTGTGTATTTTTCTCTACGCAACCTTGACC	423
QY	101	TrpSerSerLeuLeuIysAsnCysSerAspMetGlyAlaHisLeuValValIleAspThr	120
DB	424	TGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGCTCCTCTGCTGTTATTCACACA	483
QY	121	GlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgGlyGluPheTrpIleGly	140
DB	484	CAGGAAGAGCAGGAATTCCTTTTCGCACAAAACCTTAAAGGAAGAGAGTTTATATTCGA	543
QY	141	LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu	160
DB	544	CTGACAGACAGGTGGTGGAGGCTCAGTNGCATGGGTGGATGATACACCTTTTCACAGAG	603
QY	161	SerLeuSerPheTrpAspAlaGlyGluProAsn	171
DB	604	TCCTTGAGCTTCGGGATGCTGGGGAGCCCAAC	636
RESULT 12			
BY743813			
LOCUS	BY743813	643 bp	linear
DEFINITION	musculus cDNA clone 1830018A02 5', mRNA sequence.		
ACCESSION	BY743813	EST	17-DEC-2002
VERSION	BY743813.1	GI:27170082	
KEYWORDS	Mus musculus (house mouse)		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 643)		
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikiado, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tonaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusci, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perteau, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,		

US-10-812-620-2 (1-214) x BY743813 (1-643)

Qy 1 MetAenSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAenSer 20
 Db 124 ATGAATTCAACCAATCGCTGCATCCACCACACAGAGAGAGATGCTTCAAAAATCC 183
 Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
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 Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAenLeuGlnProHis 60
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 Qy 61 ArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCysCys 80
 Db 304 AGAAATATTAGGAGCTTCTCTGCTACAGTGAGGCATCAGGTTCAAGAAATGCTGT 363
 Qy 81 ProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr 100
 Db 364 CCTTTGAAGTGGAAACATATCAATCTAGTGTGTTATTTTCTCTACGACAACCTTGACC 423
 Qy 101 TrpSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValLilleAspThr 120
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 Qy 121 GlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
 Db 484 CAGGAAGCAGGAGAAATCTTTTTCGCACANAACTANAGGAAGAGTTTATATTTGA 543
 Qy 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThrGlu 160
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 Qy 161 SerLeuSerPheTrpAspAlaGlyGluProAen 171
 Db 604 TCCCTGAGCTTCTGGGATGCTGGGGGCCCAAC 636

RESULT 13

BY749488
 LOCUS BY749488 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
 DEFINITION cells Mus musculus cDNA clone F730001C01 5', mRNA sequence.
 BY749488
 ACCESSION BY749488.1 GI:27178916
 VERSION
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 671)
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
 Clothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
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 Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
 Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J. C., Reid, J., Reid, J., Ring, B. Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 124354683
 1246851
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 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multipeptide sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES

source
 1. .671
 /organism="Mus musculus"
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 +ve dendritic cells"

ORIGIN

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 Score: 808.00 Matches: 156
 Percent Similarity: 85.25% Conservative: 0
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 Query Match: 68.53% Indels: 25
 DB: 6 Gaps: 1

US-10-812-620-2 (1-214) x BY749488 (1-671)

Qy 1 MetAenSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAenSer 20
 Db 124 ATGAATTCAACCAATCGCTGCATCCACCACAGAGAGAGATGCTTCAAAAATCC 183

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DB	184	CAAGTGTCTCTCGGACGATAGCGGGCCCTCCATCTCTGTCTCAGTGGCTGTTTCATC	243
QY	41	ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis	60
DB	244	ACCAGATGTGTCGTAAACATATACGCTGCCTCTCAAAATTTCCGGGCAGAACTTTACAGCCACAT	303
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QY	74	-----GlySerVal	76
DB	364	CAGAATCATTAGCAAAAGTTTCTGGGCAATGTCTGAAGCCTTTCTCTCTTAGTGGTTCA	423
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DB	424	AGAATGTGTGTCCTTTGAACGTGGAAACATTATCAATCTAGTGTGTATTTTTTCTCTACG	483
QY	97	ThrThrLeuThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuVal	116
DB	484	ACAACCTTCACCTGGTGCATCAAG-ITAAAGAATTTGCTCAGACATGGGGGTCACTGGTG	542
QY	117	ValIleAspThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGlu	136
DB	543	GTTATTCGACACACAGGAAGAGCAGGAATTCCTTTTTCGCACAAAACCTTAANAGGAAAGAG	602
QY	137	PheTyrIleGlyLeuThrAspGlnValGluGlyGlnTrpGlnTrpValAspAspThr	156
DB	603	TTTTTATTGGACTGACACACAGGTGGTGGAGGGTCAGTGGCAATGGGTGGATGATACA	662
QY	157	ProPheThr	159
DB	663	CTTTTTCACA	671

5311916	BE311916	1032 bp	linear	EST 26-OCT-2000
LOCUS	601143328F1	NIH_MGC_14	Homo sapiens	CDNA clone IMAGE:3507103 5',
DEFINITION	mRNA sequence.			

FEATURES
SOURCE

/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into ECORI/XhoI sites using the following adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:			
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Best Local Similarity:	65.55%	Mismatches:	42
Query Match:	62.38%	Indels:	7
DB:	2	Gaps:	3
US-10-812-620-2 (1-214) x BE311916 (1-1032)			
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Qy	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
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Qy	41	ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---	59
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Qy	60	HisArgAsnIleLysGluLeuSerCysTySerSerGluAlaSerGlySerValLysAsnCys	79
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Qy	100	ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValVallIleAsp	119
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Qy	120	ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyIle	139
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Qy	140	GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr	159
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Qy	160	GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys	179
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Qy	180	AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyIle	199
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RESULT 15 BX516799 LOCUS DEFINITION BX516799 NCI CGAP Mam6 Mus musculus cDNA clone IMAGE:3158063, mRNA sequence. ACCESSION BX516799 VERSION BX516799.1 GI:32294653 KEYWORDS SOURCE Mus musculus (house mouse)			
EST 27-JUN-2003 IMAGp998247650 ;			

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 486)
AUTHORS Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D.
and Korn, B.
TITLE Mouse UnigeneSet - RZPD2
JOURNAL Unpublished (2003)
COMMENT RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Contact: Ina Rolfs
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998G247650.
RZPDLiB; I.M.A.G.E. cDNA Clone Collection;
Mouse UnigeneSet - RZPD2 (RZPDLiB No.981)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=981 Contact: Ina Rolfs
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Fax: +49 30 32639 111
www.rzpd.de

Search completed: June 9, 2005, 16:20:28
Job time : 3183 secs

FEATURES
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

Alignment Scores:
Pred. No.: 9.92e-70 Length: 486
Score: 730.00 Matches: 135
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.92% Indels: 0
DB: 5 Gaps: 0

US-10-812-620-2 (1-214) x BX516799 (1-486)
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Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
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Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
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